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RESULT
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Best Local S
Matches 307
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STRAIN-COLUMBIA;
Kaneko T., Kato T., Se
Submitted (MAR-2000) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; APO01306; BAB0302.1; ...
InterPro: IPR002955; P. Tich extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
DIACOC79F155E732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9LIE8 PRELIMINARY; PRT; 1480 AA.
Q9LIEB;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
Arabldopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traspermatophyta; Magnoliophyta; eudicotyledons; core eudicentysids (Pressential Core eudicentysids).
                                                                    432
                                                                                                                         385
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TAT---PPVAKPPVETPPIATPPTAKPPISTPPISKPPVATPPAATPPITTPTPVKPPVA
                                              TTTKSAPTTTKEPAPTTTKSAPTTPKEP--SPTTTKEPAPTTPKEPAP---TTPKKPAPT
                                                                                                VATPPTATSPIKTPPPAKPPVATPPIAKSPIATPPTATPPVATPPIEKPPVATPPTTTPP
                                                                                                                                                 TTKEPAPTTP-KEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTT----KEPSPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                          KEPAPTTT-----KSAPTTPKEPAPTTT-------KEPAPTTPKEPAPTTKE
                                                                                                                                                                                                      PAKPPVAISPIVT--PPVTPIAQPPVATPPTATPPVATPPIATPPTSKSPISTPPISESP
                                                                                                                                                                                                                                                    PA-----PTTTKSAPTTP-KEPAPTTPKKPAP--TTPKEPAPTTPKEPTPTTPKEPAP
                                                                                                                                                                                                                                                                                                         PVAAPPITNPPISKPPYTTP----PTTTPPIAKPPIATPPISTPPAATPPAATPPITTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPPPSTPK---
                                                                                                                                                                                                                                                                                                                                                                                                         TQMPPIATP-PIAKSPVATPPIATPPTATPPITIPPVATPPITTPPIANPPIIMPPIATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTS----PKITTAKPINPRPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKV--LAKPTPKAETTTKGPALTTPKEPTP--TTP--KEPASTTPKEPTPTTIKSAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPRPHPKPPNVK------PHPHPKPPTKPHPHPKPPTKHHPHPKPPTTKPPPKPPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Nakamura Y., Asamizu E., Tabata
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 800.5; DB 10; Length 1480;
Pred. No. 1.2e-45;
4; Mismatches 505; Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Embryophyta; Tracheophyta; edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 171;
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		1 1 2	RESULT
	ATPPVTNPPTAMPPIVT 1087	1071 #	Db
	YLPRVPNOGIIINPMLS 1047	1031)	Qy
	VLPPIAKPPVETSPTATPPTATPPVAIPPVVK	1026 \	ДĠ
PHVFMPEVTPDMD 1030	AMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD	978	Qy
PPVATPPIAKPPT 1025	KPPTTTPPTAT-PPVAMPPIATPPTAKPPVATPPIANPPVEKPPVATPPIAKPPT	972 1	Db
TSRIAE 977	QKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAE	929	VΩ
: PTATSPVATPPIA 971	PAKPPVAIPPIATPPVAKPPVATPPTATPPIATSPIATPPVVTPPTATSPVATPPIA 971	915	DЬ
DRATNSKATTPKP 928	QDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKP	873	Qy
\KPPVAIPPIKTPP 914	TPPITTPPPAKEPVATPPIATPPIAKPPVATPPTATPPIATSPVAKEPVATPPIKTPP	857	DЬ
(ITATTTQVTSTTT 872	TKPEMT-TTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTT	814	Qy
PPISKPPVATPPAA 856	TPPIAKPPVATPPTTAPPTATPPVAKPPVATPPIATPPTAKPPILTPPISKPPVATPPAA	797	Вb
PKEPGVPTTKTPAA 813	TPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA	756	Qу
	MPPIATPPTAKPPIATPPIATPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATBPVA 796	737	Db
KPAPTTPE 755	APKELAPTTTKGPTSTTSDKPAPTTPKETAPT-TPKEPAPTTPKKPAPTTP	705	Qy
TTIPPTATPPVA 736	KPPVATPPTATPPIATPPIATPPVATPPVATPPVATPPIAKPPTTIPPTATPPVA 736	682	Db
TTLKEPAPTTPKKP 704	KEPTSTTSDKPAPTTPKGTAP-TTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKP 704	646	Qy
PPVAIPPIATPPVA 681	TPPIATPPIAKPPVATPPTATPPIATSPVAKPPVATPPIKTPPPAKPPVAIPPIATPPVA 681	622) b
PKKPAPKELAPTTT 645	TPKEPAPTTPKEPAP-TTPKGTAPTTLKEPAPTTPKKPAPKELAPTTT 645	591	. Q
PPITTPPPAKPPVA 621	TPETATPEVAKPEVATPEIATPETAKPEISTPEISKSPVATPEAATPEITTEPEPAKEEVA 621	562	Ф
APNTPKEPAPT 590	TPEKLAPTTPEKPAPTTPEELAPTT-PEEPTPTTPEEPAPTTPKAAAPNTPKEPAPT 590	535	Qy
PPIAKPPVVTPPTT 561	TPPLAIPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATPPVATPPIAKPPVVTPPTT	502	DЪ
PKKLTPT 534	TPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT	487	Qy

Q41805
ID Q41805: PRELIMINARY; PRT; 1188 AA.
AC Q41805;
DT 01-NOV-1996 (TIEMBLTel. 01, Created)
DT 01-NOV-1996 (TIEMBLTel. 01, Last sequence update)
DT 01-NOV-1996 (TIEMBLTel. 17, Last sequence update)
DE EXTENSIN-LIKE PROTEIN PRECURSOR.

Zea mays (Malze).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cli
CR Panicoldeae; Andropogoneae; Zea.

RN [1]
RN [1]
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-B73; TISSUE-POLLEN;
RA Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; 334465; CaaR84230.1; .
DR EMBL; 34465; CaaR84230.1; .
DR Mendel; 14346; Zeama; 2358;14346.
DR InterPro; IPR003592; LRR_out.
DR STRAIL
DR STRAIL
DR STRAIL
DR STRAIL
SMART; SM00370; LRR; 4.
STRAIL
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Qy
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                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Favello A., Fulton L.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q20007;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
COSMID F35A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1243 SPPPAP--VKPPSLPPPAPVSSPPPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q20007
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                                                                                                                                                                                                                                                 Watson A., Weinstock L., Wilkinson sprodt J., Wolldwar F., 2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans."
                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                   Submitted (JAN-1996)
                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                       Nature 368:32-38(1994).
                                                                    Waterston R.;
Submitted (JAN-1996)
                                                                                                                                                                    Leimbach D.;
   Waterston R.;
                     STRAIN-BRISTOL N2;
                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTK 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ELKSSPPPAPVSSPPSAPKSSPPPAPVSLPPPEVKSSPPPAPISSPPPPAKSP----
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                                                                       ç
                                                                                                                                                        the EMBL/GenBank/DDBJ databases.
                                                                       the EMBL/GenBank/DDBJ databases.
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Matches 262
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"Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF159297; AAD5980.1; -.

InterPro: IPR001611; LRR.

InterPro: IPR001998; Xylose_isom.

InterPro: IPR001998; Xylose_isom.

InterPro: IPR002965; P_rich_extensn.

InterPro: IPR002959; LRR-Out.

Pfam: PE00560; LRR; 3.

PRINTS: PR01217; PRICHEXTENSN.

PRINTS: PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID-4577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 24.0 es 262; Conservative
SSPPMVEKTSPPPATVSSPPPTPKSSPPP---APVSSPPPVVKSSPPPAPVSSPPPTPKP
                                                                                        SVSSPPTTVKSSPPPAPLSSPPMTPKSSSPPAHVSSPPEAEKSSPPLAPISSPPSEPKSP
                                                                                                                                 PEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT
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                                                                                                                                                                                                                                                                                                                                                                     PTPPSTPSKPPPPSPVETLPPPSKSSPPEEPVSSPPQAPKSSSP-----PAPVS--Sppp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVVLPPPAKTESPPAPVASPPPEAPVSSPQPQVKSPPPPAPVASPPPPMKSP--PPPARV 583
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SM00370; LRR; 3.
CE 1315 AA; 134401 MW; 64C97A2A01F093(
                                         ----PTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT----TPKG 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 811.5; DB 10;
Pred. No. 2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64C97A2A01F0936F
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paccleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong K., Zhu S., Zhu X., Smith H.O.
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
RA Zience 287:2185-2195(2000).
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Best Local S
Matches 276
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FlyBase; FBG0002537; Chitin_binding.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR002965; P_nich_extensn.
Ffsg. FP01007; Chitin_bind_2; 2.

PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00494; ChtBD2; 2.

SEQUENCE 1795 AA; 194464 MW; 07F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Caditu E., Dreano S., Lelaure V., Mottier S., Galibert F.,
Caditu E., Dreano S., Lelaure V., Mottier S., Galibert F.,
"Sequencing the distal X chromosome of Drosophila melanogaster.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003421; AAF45644.1; EMBL; AL031028; CAA19845.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431
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                                                                     PAPTTTKKPAPTAPKEPAPTTPK-ETAPTTPKKLTPTTPEKLAPTTPEKP--
                                                                                                                TTTTTTEKPITSSPKPTTTTQKTTSTAPNTTKVAITTQKETTPTQSTSTTIFTRKTTTNN
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TIPEELAPITPEEPIPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPT-
                                                  PEPTSTEKPITSTTPKPSTTTPKTSTVASSTEKTTISSPKPTTEKSTENPTTNSVKTSAL
                                                                                                                                                 SPTTTKEPAPTTPKEPAPTTPK----
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Pred. No. 6.6e
29; Mismatches
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Smith H.O.,
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Best Local S
Matches 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYST GERMINATION SPECIFIC ACIDIC REPEAT PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                         Goernhardt B.;
Submitted (APR-1998) to the
EMBL; AF061185; AAC72308.1;
SEQUENCE 1489 AA; 164037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytophthora infestans (Potato late blight fungus) Bukaryota; Stramenopiles; Oomycetes; Pythiales; Py
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-RACE 1-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4787;
  418
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TEETPYEPTEETTYTPTEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTEET
                                                                                                                                                                                          YEPSDETEAPTEGTTY----VPREETTAAPSEDTTYAPREVTPYAPTEKPYDVEETTYVTE
                                                                                                                                                                                                                                        FERGRECDCDAQCKKYDKCCPDYESFCAEVKDN---KKNRTKKKPTPKPPVVDEAGSGLD
                                                                                           ESTYAPTKSETNAPTERMHYAHIEKPCDTEVTMYAPTEETTYAPTEETTYAPTEETTYAP
                                                                                                                                               NGDFKVTTPDTSTT----
                                                NSDT - - -
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                                 -SKETSLTVNKETTVETKETTT---TNKOTSTDGKEKTTSAKETQSIEKTSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKA-PK
                                                                                                                                                                                                                                                                                                                     12.1%;
31.8%;
                                                                                                                                                 -QHNKVSTSPKITTAKPINPRPSLP
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                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                   Score 855; pb
Pred. No. 2.7e-
52; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                       855; DB 10;
No. 2.7e-49;
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PRI Science 287, 2185-2195(2000).

DR EMBL; AE003495; AAG22353.]; -.

PRI SEQUENCE 1049 AA; 107278 MW; 954DD629E7619671 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.3%;

Best Local Similarity 34.6%;

Matches 371; Conservative 4;
 633 K----KPA-----PKELAPT-----TTKEPTSTTSDKPA---
                               531 KGTTAKPTTLK---PTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTA
                                                                                                                          471
                                                                                                                                          530 KLTPT-----TPEKLAPTTPEKPAPTTPEELAPT--TPEEPTPTTPEEPAPTTPKAAAPN 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                  314 TTPKEPAPTTTKEPAPTTTKSAPTTPKE---PAPTTPKEPAPTTPKEPAPTTPKEPT----P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 KDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTS---TTQHNKVSTSPKITTAKP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 SAKET--QSIEKTSAK--DLAPTSKVLAKPT------PKAETTTKGPALTTPKEPTPTT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 TEGTTAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEG----T 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 KPNEIGTTAKPTTLKP-------TEGTSAKPTTLKPTEGTSAKPTTLKP 71
                                                               TPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTA------PTTLKEPAPTTP 632
                                                                                                        {\tt TLKPTEGTTAKPTTLKPTKGTKGTSAKPTTLKPTEGTTAKPTTLKPTEGTTAKPTTLKPT}
                                                                                                                                                                                 --PTTLKPTEGTTAK----PTTLK-PTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPT
                                                                                                                                                                                                       PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPA---PTAPKEPAPTTPKETAPTT--PK 529
                                                                                                                                                                                                                                                         TTAK---PTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAK- 416
                                                                                                                                                                                                                                                                                              TTPKEPAPTT-----TKSAPTTTKEPAPTTTKSA---PTTPKEPSPTTTKEPAPTTPKE 474
                                                                                                                                                                                                                                                                                                                                  TTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTDG
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                                                                                                                                                                                                                                                                                                                                                                                                           TTAK----PTTLKPTEGTTAKPTTLNPTEGTSAKPTTLKPTEGTTAKPTTLNPTEGTSAKP
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Pred. No. 6.3e-55;
5; Mismatches 439;
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------PTTPKGT 664
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., Mattei B., McIntosh T.C., McLeod M.P., McPherson	B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z	owland T.J., Wei MH., Ibegwam C.,	A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., N.L., Harvey D., Heiman T.J., Hernandez T.R., Houck T.	N.J., Evangelista C.C., Ferraz C., Ferriera S., Fleisch C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser H	dson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn p	erry J.M., Cawley S., Dahlke C., Davenport L.B., Davies p.,	K.C., Busam D.A., Butler H., Cadien F., Brottler P.,	Berman B.P., Bhandari D., Bolshakov S.,	n HJ., Andrews-Pfannkoch C	er E.G., Helt G., Nelson C.R., Miklos G I G	Yandell M.D., Zhang Q., Chen L.X.,	R.A., Lewis S.E., Richards S., Ashburner M., Henderson of	iker S.E., Holt R.A., Evans C.A., Gocayne J.D.	NE=20196006; PubMed=1	TRAIN=BEDDOT EV.	 Weoptera; Endopterygota; Diptera; Brachycera; Mus Drosophilidae; Drosophila	aryota; Metazoa; Arthropoda; Tracheata; H	56G7.1 OR sophila m	56G7.1 PROTEIN.	01-WV-1999 (TrEMBLrel: 08, Created) 01-WV-1999 (TrEMBLrel: 12, Last sequence update)	NOV-1000 (manager) 00	076894 PRELIMINARY; PRT; 1795 AA.	T 7	TLKPTEGTTAKPTTLKP	TSRIAEAMLQTTTRPNQTPNSKLVEVN		KPTTLKPTEGTTAKPTTIKPTEGPAKPTTIKPTTAKPTTAKPTTAKPTTAKPTTAKPTTAKPT	TPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPPTDBKMTSTMD	SAKPTTLKPTEGTTAKPTTLKPTDGTTAKPTTLKPTEGTSAKPTTLKPTE 93	859 KITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKD 916	I II EGTTAK 87	816 PEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTES 858	KPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPTERTSAQPTTLK	AEPTPKALENSPKEPGVPTTK	AKPTTLKPTEGT	PKEPAPTTPKKPAPTTPETPPPTTSEVSTPT-TTKEPT 7	TTAKPTTLKPTDGTTAKPTTLNPTEG 7	T 72	

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Best Local Similarity
Matches 330; Conserv
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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Waterston R.;

Waterston R.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC006797; AAF60743.1; -.

EMBL; AC006797; AAF60743.1; -.

ENDED: TRO02965; P.Tich_cxtensn.

PRINTS; PRO1217; PRICHEMIN.

SEQUENCE 1079 AA; 110532 MW; 8DBDE3824CF80CA1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                       TOSIEKTSAKDLAPTSKVLAKPTPKAETT-TKGP-ALTTPKEPTPTTPKEPASTTPKEPT
                                                                                                                                                                         TTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPET
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                                                                                                 EPAPTTTKKPAPTAPKEP---APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEEL
                                                                                                                         TRTEPPSSSTTPVQNTTTTAPETTSTEPPSSSTTPVQTTTTT----APETTSTEPPSSST
 TTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKP-APTTPKGTAPTTPKEP
                        PETTSTEP-PSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPE-TTSTESPSSS
                                                APTTPEEPTPTTPEEPAPTTPKAAAPNTPKEP--APTTPKEPAPTTPKEPAPTTPKETAP
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29.5%;
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EMBL/GenBank/DDBJ
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Pred. No. 2.9e
29; Mismatches
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?.9e-57;
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Q9N4S7 Q9N4S7; 01-OCT-2000 01-OCT-2000

(TrEMBLrel.

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Pfam; PF00045; hemopexin; 2.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
SMART; SM00120; HX; 2.
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SChumacher B.L., Hughes C.E.,
Aydelotte M.B.;
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EMBL; AF056218; AAD13404.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
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                                                                 ALSIAQYKSRPESYYFFKRGGSVQQYTYKQEPTQKCTGRRPAINYSVYGETAQVRRRRFE
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2000 (TrEMBLrel. 15, Createu,
01-OCT-2000 (TrEMBLrel. 15, Last sequence update,
01-JUN-2000 (TrEMBLrel. 17, Last sequence updat
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InterPro; IPR000585; Hemopexin.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR001212; Somatomedin_B.
Pfam; PF01033; Somatomedin_B: 2.
PRINTS; PR010217; PRICHEXTENSN.
PRINTS; PR001217; PRICHEXTENSN.
PRINTS; PR00122; SOMATOMEDINB.
SMART; SM00120; HX; 2.
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SMART; SM00201; SO; 2.
SMART; SM00224; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS000524; SOMATOMEDIN_B; 2.
SPOSITE; PS00524; SOMATOMEDIN_B; 2.
SEQUENCE 1054 AA; 115991 MW; 4FC64BFA
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                                      NKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTINKQTSTDGKEK
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PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE: PS00524; SOMATOMEDIN_B; 2.
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SMART; SM00201; SO; 2.
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Pred. No. 0;
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RESULT
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                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                   O9BX49;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BG174L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR).
BG174L6.2.
                                                                                                                                                                                 SEQUENCE FROM N.A.
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Pred. No. 0;
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MW; 782A11746B3FI
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Q9i7s1 drosophila
Q76894 drosophila
Q964449 phytophtha
    O96449 phytophthor
O969m0 zea mays (m
O20007 caenorhabdi
O91ie8 arabidopsis
O41805 zea mays (m
p70670 mus musculu
O9vel9 drosophila
O99iq96 chlamydomon
O9vpg1 drosophila
O57580 gallus gall
O99jltl rattus norv
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Q9jm99 mus n
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Q9n4s7 caenos
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ALIGNMENTS

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RESULT
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEGAKARYOCYTE STIMULATING FACTOR.
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SEQUENCE FROM N.A.

Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A Turner K.J., Fitz L.J., Calvetti J., FitzGerald M., Kriz M.J. Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J. Fraser H., Bean K., Norton C.R., Gesner Bhatia S., Kriz R., Hewick R., Clark S.C.;

Blood 78:279-279(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          Turner K.J., Fitz I.J., Temple P., Jacobs K., Larson D., Leary A.C., Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U70136, AAB09089 1; -.

EMBL; U70136, AAB09089 1; -.

InterPro; IPR000585; Hemopexin.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR002400; GFcysknot.

InterPro; IPR002400; GFcysknot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                        Jacobs K., Turner K.;

(In) Preissner K.T., Rosenblatt S., Kost C., W., Mosher D.F. (eds.);

Biology of vitronectins and their receptors.,

plsevier Science Publishers B.V. (1993).
                                                                                                                                                                                                                                                                                                                           Merberg D.M., Fitz L.J., Temp
FitzGerald M., Scaltreto J.,
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pfam; pF00045; hemopexin; 2.
pfam; pF01033; Somatomedin_B; 2.
pRINTS; pR00438; GFCYSKNOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   Temple P., Giannotti J., Murtha
J., Kelleher K., Preissner K., F
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                                                                                                                                                                                                                                                                                                       Wegerhoff J.,
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, Kriz M.J.,
p. Gesner T.,
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Š 밁 Ş 밁 õ 밁 Ş 밁 δ ₽ Š 밁 δ 망 Š В Š В Š g Ş 망 Ş В δ В Ş В 638 aq-epvttqel---iatqepsttqehadekkasegdnislsrlseeteekshtkkkkssw 672 PETPPPTTSEVSTPTTTKEPTTIHKSPDE-----STPELSAEPTPKA------694 lkfgrgnkndkksknekkpslesvkqnådeqkeqptdsqlsvnaqdsvtigeptatqepp 753 531 471 lttqepvtaqepvttqeliatqepsttqehadekkasegdnislsrlseeteekshtkkk 530 500 NTPKEPA----PAPTTPKE----PAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPK 551 440 440 ETAPTTPKKLTPTTPEKLAPTTPEEKPAPTTPEELAPTTPEEEPAPTTPKAAAP 499 381 gnkndkksknekkpslesvkqnadeqkeqptdsqisvnaqdsvtiqeptatqep-pttqe 439 387 324 348 184 ASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPA----P 239 270 vttqepvt1eepvtt----qepvt1ee--pvttqepvt1eepvttqepvttqepvttqep 323 228 vtvqep---vtsqepvtpqe-----pvtpqe--pvtpqe--pvtpqepv-ttqep 269 240 TTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTTKEP 299 130 nsnqnkeinev-kessqtqppv-----tpqetvttq--aaatpqetvetqepvtieep 179 ksswlkfgrgnkndkksknekkpslesvkqnadeqkeqptdsqisvnaqdsvtiqeptat 590 KPAPKELAPTITKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTL 611 lta-----tylegeptttge----tylegeptttge----tylegeptttge----tylegep 470 ---vttqepvttqepvtveehidekkgsegdnislsslseeteekshtkkkksswlkfgr 380 APTITKSAPTITKEPAPT----- 386 A----PTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPA----PTTTKEP----SPTTPKEP 347 KTITTTEIMNKPEETAKPKDRATNSKATTPKPQK 848 ttqeltatqeptttqe---tvteqeptttqetvtaqepittqepvtaqepvttqellatq 810 MTKETATTTEKTTESKITATTTQVTSTTTQDTTPFK--ITTLKTTTLAPKYTT-----TK 814 ------LENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPE-TTTAAPK 761 -----PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPK 439 KTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPT----PTTPKEP 183 693 713

Search completed: April 26, 2002, 16:24:09 Job time: 439 sec

811 epsttge--hadekkasegdnislsrlseeteek 842

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This novel 55 kDa protein is encoded by an open reading frame a Mycobacterium tuberulosis DNA fragment (see AAT93610) contain polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proline rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAW31851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA and related proteins or RNA derived from M. tube used for diagnosis of mycobacterial infections, monitori vaccination and development of anti-mycobacterial agents
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mpalp--pappsppatrlcpplppsppapnsp--pappap---
                            TPTTPEEPAPTTPKA---AAPNTPKEPAPTTPKEPAPTTPK---ETAPTTPK
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                                                                                                                                      KPAPTAPKEPAPTTPKETAPTTPKKLTPTTPE--KLAPTTPEKPAPTTPEELAPTTPEEP
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ilarity 30.6%;
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Pred. No. 5.5e-29;
9; Mismatches 253
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infections, monitoring
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IQQVSSVKDNKKN--RTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPK 76

Query Match
Best Local Similarity
Matches 249; Conserv

Conservative 117;

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11-SEP-1984;
10-SEP-1985;
                The inventors claim a novel DNA molecule which comprises nucleotide sequence corresp to all or a portion of the k sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA antigenicity suitable for providing protective immunity plasmodium falciparum malarial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP60570 standard;
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                                                                                 Disclosure;
                                                                                                    poly:peptide(s) having
falciparum
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                                                                                                                                                                                                                                                                                                                          Plasmodium
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Sequence
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                                                                                                               for Plasmodium falciparum antigens - expressing
de(s) having antigenicity of RESA or FIRA antigens
844 AA;
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                                                                                Fig 7; 55pp; English.
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84AU-0007066.
85AU-0047326.
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ARESULT 1
AAVS 3666
ID AAVS 366
                                                                                                                                                                                                           The present sequence is obtained from a clustral X alignment with CC protein 608. Protein 608 was identified using the method of the invention CC after subjecting rat osteoblasts to mechanical stress. Expression of the CC defendance of the protein for the CC defendance of the specification describes a method for the CC defendance of genes responsive to a specific mechanical stress. The CC method comprises applying the mechanical stress to an organism (tissue CC or cells comprising bone cells), isolating the specific cellular comprising bone cells), isolating the specific cellular companism (the method is used to identify genes and extracting mRNA from them, and differentially analysing the GC genes whose expression is responsive to a specific stress. The identified disease state. The risk determination methods are used for testing a controlling a physiological or the method of the invention, are used for treating or controlling a physiological or disease state (specially osteoporosis or the methods of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or its symptoms or other factors causing or contributing to osteoporosis or controlling a physiological or disease state (especially osteoporosis or its symptoms or other conditions involved in mechanical stress or its bone development.
         Query Match
Best Local Sin
Matches 225;
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                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of stress induced genes for determining preventing, treating or controlling osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-053304/04.
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Pred. No. 8.3e-29;
6; Mismatches 379
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Similarity 26.2 25; Conservative

66;

379;

Indels 169;

Gaps

40;

Tuberculosis; mycobacteria;

infection; diagnosis;

Mycobacterium tuberculosis 55 kDa protein.

XXX DXX AXX ID

27-APR-1998 AAW31855;

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entry)

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AAW31855 standard; Protein;

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                                                                                KPKDRATINSKATTPKPQKPTKAPKKPTS--TKKPKTMPRVRKPKTTPTP-----RKMTST
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                                                                                                                                                                                                                                                                                                           18-APR-1997;
                                                                                                                                                        Espitia C,
                                                                                                                                                                                                      (GBFB ) GBF GES BIOTECH FORSCHUNG
New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring
                                                                              N-PSDB; AAT93610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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Local Similarity 28.2%;
hes 248; Conservative 3
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                                                                                                                                       KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSP----DESTPELSAEPTPKA--LENSP 718
                                                                                                                                                                        KEPAPTTP----KKPAPKELAPTTTKGP-TSTTSDKPAPTTPKET----APTTPKEPAPTTP 664
                                                                                                                                                                                                                                           --pippgkpwttpplapappepk-tvpvlppgpscppsekpnppappeppepksspalpp 488
                                                                                                     --pappapptppklls--anppcppvppapnrppappappappelpappdpptppvansp
TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATN 838
                                                                KEPGVPTTKIPAATKPEMTTTAKDKTIERDLRTTPETTTAAPKMTKETATTTEKTTESKI 778
                                 --pappappappsalpfvnppa-----pptpaapk--
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; pred. No. 5.3e-35;
39; Mismatches 361;
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26-MAY-2000;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                            29-JAN-2001; 2001WO-US00661
                                                                                                                                                                        Нолю
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                                                                                                                                               WO200157270-A2
                                                                                                                                                                                             inflammatory
                                                                                                                                                                                                          Probe; human;
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2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                              breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                   Protein;
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                                                                                                                                                                                      proliferative breast disease;
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in nucleic acid expressed in the human breast. The probes at useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic infiammatory diseases include: breast cancer, disorders of development, breast diseases of the breast, fibrocystic changes, proliferative, breast diseases and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed at for this patent did not form part of the printed at for with includes in electronic format directly from WIPO
                        at ftp.wipo.int/pub/published_pct_sequences.
 Sequence
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by protein-protein interactions between domains designated dockerins can and cohesins, which are found on the catalytic and scaffold subunits can and cohesins, which are found on the catalytic and scaffold subunits can compare in the callulosome degrading compositively. An example of such a complex is the cellulosome degrading compositively. An example of such a complex is the cellulosome. This complex from Clostridium thermocellum, known as the cellulosome. Compositively complex comprises around 15 proteins including endoglucanases, which complex complex comprises around 15 protein designated the cellulosome compositively complex comprises a protein designated the cellulosome compositively co
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                                                                                                                                                                                                                                                                           TKSAPTTPKEPAPTTTKEPAPTTPKEPA----PTTTKEPAPTTTKSAPTTPKEPAPTTPK 266
                                                                                                                       sdeptpsdeptpsdeptpsetpeepiptdtpsdeptpsdeptpsdeptpsdeptpsdept
                                                                                                                                                     TTPKEPA--PTTTKEPSPT-TPKEPAPTTTKS-APTTTKEPAPT---TTKSAPTTPKEPS
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                                                                                                                                                                                                    KPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPT-TPKEPAPTAPKKPAPTTPKEPAP 325
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                              APT---TPKETAPTTPKKLTPTTPEKLAPTTPEKPAPT---TPEELAPTTPEEPTPT-TP 486
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Pred. No. 1.1e-48;
4; Mismatches 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gngpfglcydykirvnccwpmdkcittpsppttttpsppttttttlpptttpspptt----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttppptttpspptttpitpptstttlpptttpsppptttttppptttpsppttttpsppt 1590
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                                                                                                                                                                                                                                 TTPKEPAPT-TPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKP
                                                                                             tptptptgtqtptttpitttttttptptptgtqtpt-ttpittttttvtptptgtqtpt
DKTTERDLR---TTP--ETTTAAPKMT---KETATTTEKTTESKITATTTQVTSTTTQDT
                                    t---tpitttttvtptptptgtgtqtptttpittttttvtptptptgtgtgtptttpitttttvt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; score 1168; DB 22;
; Pred. No. 3.7e-61;
53; Mismatches 448;
                                                                                                                                                                                                                                                                                                                                                      ----TTPEKLAPTT
                                                                         ---GVPT-TKTPAATKPEMTTTAK
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                                                                                                               28-APR-1999
30-APR-1999
30-APR-1999
04-MAY-1999
05-MAY-1999
06-MAY-1999
06-MAY-1999
07-MAX-1999
11-MAY-1999
11-MAY-1999
                                                                                                                                                                                                             25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG38942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 48115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG38942 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                         termination sequence
                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
       20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ptptptgtqtptttpltttttvtptptptgtqtptttplttttttvtptptp-tgtqtptt 2243
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                                                 99US-0127462.
99US-0128744
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This sequence represents the human megakaryocytopoientin (MPO) protein. This sequence was purified using a carrier which can couple wheat germ agglutinin and heparin to separate MPO. Fragments of this sequence (see C AAR80039 and AAR80040) were used to produce the amplification primers can then be used as probes to screen human cDNA libraries for MPO cDNA. CC transform cells to produce MPO. The MPO sequence is capable of promoting colony formation of megakaryocytes, enlarging the size of megakaryocytes and stimulating the proliferation of multipotential stem cells. The CC and stimulating the proliferation of multipotential stem cells. The CC serums of patients with aplastic anaemia, and from animal blood or urine cc by radiation exposing the animals to induce aplastic anaemia.
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.2
                              169
                                                         241
                                                                                   109
                                                                                                               181
                                                                                                                                                  121 ppsgasqt1ksttkrspkppnkkktkkvieseeitevkdnkknrtkkkptpkppvvdeag
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                         49
                                                                                                                                                                                                       61 krvctaelsckgrcfesfergrecdcdaqckkydkccpdyesfcaevhnptsppsskkap 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New haematopoietic cell growth factor - used for treating thrombocytopenia and hematocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHAN-) SHANGHAI BEITI BIOTECHNOLOGY CO LTD
                                                                                                                                                                                              25
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                                                                                                                                                                                                                                                         WO9523861-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                            1 MAWKTLPIYLLLLLSVFVIQQVSS-----
LTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKE
                                                      VETKETTTTIKOTSTDGKEKTTSAKETOSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 168
                                         vetkettttnkqtstdgkekttsaketqsiektsakdlaptskvlakptpkaetttkgpa
                                                                                             {\tt sgldngdfkvttpdtsttqhnkvstspkittakpinprpslppnsdtsketsltvnkett}
                                                                                                            SGLDNGDFKYTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1995-320576/41.
                                                                                                                                                                                                                                                                                                                                                                                                   452
                                                                                                                                                                              ----VKDNKKNRTKKKPTPKPPVVDEAG
                                                                                                                                                                                                                                                                                                                                                                                                   Α,
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393..396
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                                                                                                                                                                                                                                                                                                                           Ψ
                                                                                                                                                                                                                                                                                                                                    Score 1397.5;
Pred. No. 4.8e
                                                                                                                                                                                                                                                                                                                         Mismatches
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nes 21;
                                                                                                                                                                                                                                                                                                                                              DB 16; Length 452;
                                                                                                                                                                                                                                                                                                                Indels 143; Gaps
                                                                                               240
                                           300
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the polynucleotides (II) that encode them: (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and CC associated with inappropriate colon tumour associated protein (TCAP) ce expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by ce expression, such as colonic cancer. For example, (I) and (II) may be rectivitying mutations or deletions in a patient's genome that affect the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complements the presence of similar nucleic acids in samples, and continued the presence of similar nucleic acids in samples, and continued the patients may be in need of restorative therapy. (I) may be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used to down regulate cas diagnostic agents for detecting the presence of TCAPs and activity. The anti-(I) antibodies may also be used to down regulate used to applicate the presence of the presence of TCAPs and activity. The anti-(I) antibodies may also be used to down regulate the presence of TCAPs and presence of TCAPs in samples.
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ID AAM2
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                                                                                                                                                                                                                                                                                                                                                                                              Colon tumor associated proteins and nuc prevention, diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
28-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-441847/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-2000; 2000WO-US35596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C899P predicted amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM24516 standard; Protein; 5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2001
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lmmunogenic; gene the;
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m lttpkeptpttpkepasttpkeptpttiksapttpkepaptttksapttpkepaptttke}
                                                                                                                                                                                                                                                                                                                     present invention describes colon tumour associated proteins (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GE,
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                                                                                                                                                                                                                                                                                                                                                            2; Page 446-462; 472pp; English.
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E, Wang T,
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2000US-0480321
2000US-0504629.
2000US-0519444
2000US-0575251.
2000US-0609448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secrist H,
, Jiang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      upy; diagnosis; colon cancer; colon tumour;
therapy; vaccine; colonic cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                           nucleic acids useful of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meagher MJ,
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PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK 564

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RESULT
AAB60569
ID AAB6
XX AAB6
AC AAB6
XX 27-A
XX BOVI
DE BOVI
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                                                                                                                                                                                                                                                                                                                                                                                                     Bovine; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; superficial zone protein; SZP; MSF orthologue; synovial lubricant; osteopathritis; joint lubrication; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60569 standard; Protein; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine MSF orthologue, superficial zone
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                                                                                                                                                         23-JUL-1999;
19-JUL-2000;
                                                                                                                                                                                                                                                                           01-FEB-2001
                                                                                                                                                                                                                                                                                                                     WO200107068-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              860
                                                                                                                                                                                                                              21-JUL-2000;
                     WPI; 2001-182721/18
                                                                                                            (UYCA-) UNIV
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                                                                                                                   CASE
                                                                                                                                                           . 99US-0145328.
2000US-0145328.
                                                                                                                                                                                                                                2000WO-US20002
                                                                                                                   WESTERN RESERVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SZP).
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The invention relates to a method of treating osteoarthritis via the cadministration of a composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. CC of the invention may further comprise a local anaesthetic. The composition cc of the invention may be administered via intra-articular or intravenous of injection. The human CACP protein is identified in the invention as cc injection. The human CACP protein is identified in the invention as cc period (MSF) is located on chromosome 1925-31, and mutations in cc CACP protein (MSF) is located on chromosome 1925-31, and mutations in cc period (MSF) is located on chromosome 1925-31, and mutations in cc protein (MSF) is located on chromosome 1925-31, and mutations in cc protein (MSF) is located on chromosome 1925-31, and mutations in carbinate vidence of inflammation. CACP protein (MSF) cc phyperplasia without evidence of inflammation. CACP protein (MSF) cc phyperplasia without evidence of inflammation. CACP protein (MSF) cc applied to reduce the symptoms of osteoarthritis. The composition may be considered to the symptoms of osteoarthritis (e.g., joint pain, carbinate tissue and carbinate tissue and cots as a synovium lubricant, and can be used to lubricate tissue and cots as a synovium lubricant of osteoarthritis. The composition may be considered to the symptoms of osteoarthritis (e.g., joint pain, carbinate vidence cots of range of movement or joint damage). The present sequence cots protein (x20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 4; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, v
                                                                        protein (SZP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or as lubricants of tissue and joints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
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Sequence

472 AA;

DB 22; Length 472;

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В Qy B Q δÃ 밁 Qy Qγ B Qγ 멍 δõ B Matches Query Match Best Local Similarity 1011 1071 135 832 PKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRK-MTSTMPELNPT 890 1191891 194 951 254 434 s-lpeamiqtttrptptpnseiidvnsenedgdaaegekphmifrppvltpivipgteii 193 SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL 950 pkgratnsqvttpkpqkptkapkkptstkkprt-prvrkpkttptppktttsampeptpt 134 TEVWGIPSPIDTVFTRCNCBGKTEFFKDSQYWRFTNDIKDAGYPKPIEKGEGGLTGQIVA 1070 319; DYYAFSKDOYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1229 $\verb|aislagy| ksrpesvy ffkrggsvqgy| tykqeptqkctgrrpainysvygetaqvrrrrfe|$ ALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFE 1130 RAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGY 1190 dyyalskdqyynidvpsrtaraittrsgqtlsntwyncp ${\tt raigpsqvhtirihytpvrvpyqdkgflhnevkvstlwrglpnvvtsaislpnirkpdgy}$ Conservative 26.0%; Score 1707.5; DB 79.9%; Pred. No. 1.5e-94; 24; Mismatches 53; Indels ω •• Gaps

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AAR80041 standard; Protein; 452
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AA.

AAR80041; 10-APR-1996 (first entry)

Human megakaryocytopoientin protein

RESULT
AAR80041
ID AAR8
XX
AC AAR8
XX
AC AAR8
AC Huma
XX
DT 10-1
XX
XX
UM Huma
KW megg Human; megakaryocytopoientin; wheat germ agglutinin; heparin; megakaryocyte; aplastic anaemia; thrombocytopenia; hematocytopenia; multipotential stem cell.

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RESULT
AAB29778
ID AAB2
XX AAB2
XX AAB2
XX AAB2
XX AAB2
XX Huma
XX Huma
XX Huma
XX Oste
KW fric
KW fric
KW fric
KW oste
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23-APR-1999;
                                                                                                                                                                                                                         Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic;
                                        24-APR-2000; 2000WO-US10953,
                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                      Human MSF-derived tribonectin.
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Novel tribonectin polypeptide useful as lubricant for treating related to the sequence of the control of the formative splicing of the human MSF (megakaryocyte stimulating factor) of a motif having at least one o-linked oligosaccharide control control faving at least 50% identity to the sequence KEPAPT (MAR29774). The invention also relates to a nucleic acid encoding a human tribonectin for inhibiting tissue adhesion formation; and a method control for diagnosing osteoarthritis or a predisposition to osteoarthritis by continuant, wherein an increased amount of MSF compared to a control contendant, wherein an increased amount of MSF compared to a control contendant of osteoarthritis. The tribonectin and DNA encoding it are useful in the manual, wherein an increased amount of MSF compared to a control contendant of indicates the presence of or predisposition to osteoarthritis. The tribonectin and DNA encoding it are useful in the manual, one of the surfaces is a membrane, foam, gel or fibre, is cused of indicates the presence of or predisposition to obtain the indicates the presence of or predisposition to obtain a hological sample of a control contendant of indicates the presence of or predisposition to developing contendant of indicates the presence of or predisposition to developing contendant of indicates the presence of or predisposition to obtain the indicates the presence of or predisposition to obtain the indicates of the surface of the surfaces of the surfaces such as the injured of the surfaces is pericardial tissue. DNA encoding a substantial portion of a human MSF-derived tribonectin. The present sequence represents sequence of the surfaces is pericardial tissue. DNA encoding a substantial portion of a human MSF-derived tribonectin.
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Š 밁 Q В Ş В Q 밁 δõ В δÃ 밁 Qy 밁 Query Match Best Local S Matches 794 445 336 385 282 325 .173 229 265 205 121 145 85 PRESLPENSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK 144 61 prps1ppnsdtskets1tvnkettvetkettttnkgtstdgkekitsaketgs1ektsak 25 VKDNKKNPTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPIN 1 vkdnkknrtkkkptpkppvvdeagsgldngdfkvttpdtsttqhnkvstspkittakpin TPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTDEEPTPTTPEBDAPTTPKAAAPNTPKE t-kepapttkep-apttke-paptt-kepaptt-kepaptt-kepaptt-ke PAPTTEKEPAPTTPKKPAPTTEKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPT ptt-kepap-ttkepaptt-kepapttkepap-ttkepapttkepaptt-kepap-ttke PTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE -kepaptt-kepaptt-kepaptt-kepapttkepaptt-kepaptt-kepaptt-kepa paptt-kepaptt-PKKPAPTTPKEPAPTTPKEPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPA epaptttksapttpkepap-ttkepaptt-kepap-ttkepapttkepaptt-kepaptt dlaptskvlakptpkaetttkgpal-----ttpkepasttpkeptpttlksapttpk DLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTTKSAPTTPK 204 Similarity Conservative -kepaptt-kepaptt-kepap-ttkepaptt-kepaptt-kepapt 53.0%; Score 3484; DB 2 74.6%; Pred. No. 2e-200; tive 28; Mismatches { DB 22; 60; Indels 162; Length 902; Gaps 388 384 281 324 228 264 172 60 84 66;

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                                                                                                                                                                                       Human; sheep; plg; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
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 25-JAN-2000;
17-JUL-2000;
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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating molety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a
                                                                                                                                                                                                                              Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety
                                                                                                                                                                                                   Claim
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cc numan tribonectin for inhibiting tissue adhesion formation; and a method cc of diagnosing osteoarthritis or a predisposition to osteoarthritis by cc mammal, wherein an increased amount of MSF compared to a control cc indicates the presence of or predisposition to developing cc osteoarthritis. The tribonectin and DNA encoding it are useful in the cc treatment of osteoarthritis, where they may be used for lubricating cc mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formalisted as a membrane, foam, gel or fibre, is cuseful for inhibiting adhesion between two surfaces such as the injured or trauma, or an artificial device e.g., an orthopaedic implant. In tribonectin may be used in gene therapy. The present sequence represents thuman MSF.
                                                                                                                                                                                                                                                                                                                                                                                   MSF-derived tribonectin; a biocompatible cotribonectin for inhibiting tissue adhesion
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                                  The invention relates to a method of treating osteoarthritis via the CC administration of a composition comprising the camptodactyly-arthropathy-CC administration of a composition comprising the camptodactyly-arthropathy-CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. CC rhe composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous conjection. The human CACP protein is identified in the invention as conjection of the invention as conjection of the symbol of the invention as conjection of the invention as in conjection of the invention of interventions in the invention of camptodactyly-cc arthropathy-coxa vara-pericarditis, in which patients have synovial conjection without evidence of inflammation. CACP protein (MSF) conjection in the treatment of osteoarthritis. The composition may be conjected to reduce the symptoms of osteoarthritis (e.g., joint pain, conjection of conjection of the symptoms of osteoarthritis (e.g., joint pain, conjection). The present sequence is not given in its entirety in figure 4 of the specification, although a GenBank accession number was given. This composition may be specification, although a GenBank accession number was given. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB60568 standard; Protein; 1404 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB60568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human megakaryocyte stimulating factor (MSF, CACP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, us treating osteoarthritis, or as lubricants of tissue and joints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1999; 99US-0145328.
19-JUL-2000; 2000US-0145328.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page -; 34pp; English.
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Sequence

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Ouery Match 98.5%; Score 6470.5; DB 22; Lee Badt Local Similarity 87.5%; Pres 20; Mismatches 1229; Conservative 0; Mismatches 0; Indeb Ratches 1229; Conservative 0; Mismatches 1229; Mism																			
Duery Match Best Local Similarity 87.5%; Score 6470.5; DB 22; Best Local Similarity 87.5%; Pred. No. 0; Mismatches 121 Part Similarity 87.5%; Pred. No. 0; Mismatches 61 kivotaelsckgrcfesfergreddagckkydkocpdyesfdae 25																			
Docal Similarity 87.5%; Pred. No. 0; 1 MANWTLPIYLLLLSVEVJQOVSS	Qу	ОУ	Qу Db	Qy	Фу	Qу	. Qy	Оy	ОУ	QУ	Оy	Qy Db	Qу	Qy Db	Db	VQ V	P 99	Qy Db	~ u a
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Claim 1, 2 and 3; Fig 1; 87pp; English.
                                                                                                                                                             New human mega-karyocyte stimulating factors - for treating immune deficiencies, cancer, exposure to radiation or drugs, bacterial and viral infections, etc.
                                                                                                                                                                                        WPI; 1992-284660/34.
N-PSDB; AAQ27223.
                                                                                                                                                                                                       Clark SC, Gesner TG,
                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                               18-JAN-1991;
10-SEP-1991;
                                                                                                                                                                                                                                               17-JAN-1992;
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91US-0757022.
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/label= Exon_x
1331..1373
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1373..1404
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                                                                                                                                                                                                                                                                               Exon_XII
                                                                                                                                                                                                      Jacobs K,
                                                                                                                                                                                                     Turner K;
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The sequence given is a full length translation from the megakaryocyte CC stimulating factor (MSF) precursor. The sequence covered by exons II, CC sequence is modified by the addition of an N-terminal sequence encoding CC terminating codon following exon IV. The cDNA sequence given contains CC (meg-CSF). Exon I contains the initiating methionine proceeding exon II and a CC (meg-CSF). Exon I contains the initiating methionine, and encodes a concoding the original meg-CSF includes exons II-IV and is thought to colory stimulating factor CC classical mammalian protein secretion signal sequence. The sequence CC primary transcript of this gene may be cleaved in different ways to CC yield a family of mRNA's each encoding a different MSF protein. Exons CC are also implicated in the stability, folding and processing of the colory signal sequence of implicated in the stability, folding and processing of the Synergy of MSF with other cytokines. Exons V - XII are believed to be sequences which direct proteolytic cleavage, adhesion, organisation of the seculular matrix or extracellular matrix processing. Both naturally couring and top-reason may be characterised by carlous combinations of alternatively spliced exons from this sequence, members of the exons spliced together in differing orders to form different colors.

Sequence 1404 AA,

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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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RESULT AAR26049

AAR26049 standard; Protein; 1404 AA.

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Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing.
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CC factor, ie. one or more of these exons may contain sequences which CC direct proteolytic cleavage, adhesion, organisation of the cellular CC matrix or extracellular matrix processing. Both naturally occurring CC and non-naturally occurring MSF's may be characterised by various CC combinations of alternatively spliced exons from this sequence, with CC the exons spliced together in differing orders to form different XX sequence 111 AA;

Query Match B.4%; Score 613; DB 13; Length 111; Best Local Similarity 100.0%; Pred. No. 8.1e-28; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 104; Conservative 0; Mismatches 0; Indels 0; Gaps 105; Indels 104; Conservative 0; Mismatches 0; Indels 0; Gaps 105; Indels 106; Gaps 106; Indels 106; Indels
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Search completed: April 26, 2002, 16:25:34 Job time: 524 sec

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                                                                                                                  The precursor cDNA sequence contains sequences derived from human megakaryocyte colony stimulating factor (meg-CSF). Exon I contains the initiating methionine, and encodes a classical mammalian protein secretion signal sequence. The sequence encoding the original meg-CSF includes exons II-IV and is thought to terminate in the region between amino acid residues 134 - 147. The primary transcript of this gene may be cleaved in different ways to yield a family of mRNA's each encoding a different MSF protein. Exons V and VI are thought to be encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encoding the different ways to yield a family of mRNA's each encodi
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stability; pro
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encoding a different MSF protein. Exons V and VI are thought to be related to the activity of the factor and are also implicated in the stability, folding and processing of the molecule. These exons are also thought to play a role in the observed synergy of MSF with other cytokines. Exons V - XII are believed to be implicated in the processing or folding of the appropriate structure of the resulting
                                                                                                                                                                                                                                                                                                                MSF-precursor (see also AAR26050).
                                                                                                                                                                                                                                                                                                                                                 The sequence covered by exons II, III and IV encodes megakaryocyte stimulating factor (MSF). This sequence was used to produce MSF a fusion protein with thioredoxin. This sequence was derived from
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10-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune deficiencies, cancer, exposure bacterial and viral infections, etc.
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Best Local Similarity
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851 KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI
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Pred. No. 1.2e-32;
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                                                                                                                                                                                                                  Identification of stress induced genes for determining risk preventing, treating or controlling osteoporosis \,\cdot\,
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CC The present sequence is obtained from a clustral X alignment with CC protein 608. Protein 608 was identified using the method of the invention CC after subjecting rat osteoblasts to mechanical stress. Expression of the CC 608 gene was found to be upregulated by about 3-fold in cells subjected CC identification of genes responsive to a specific method for the CC identification of genes responsive to a specific mechanical stress. The CC method comprises applying the mechanical stress to an organism (tissue CC or cells comprising bone cells), isolating the specific cellular CC fractions and extracting mRNA from them, and differentially analysing the CC genes whose expression is responsive to a specific stress. The identified CC genes whose expression is responsive to a specific stress. The identified CC genes whose expression is responsive to a specific stress. The identified CC genes whose expression is responsive to a specific stress. The identified CC disease state. The risk determination methods are used for testing a cc medicament for gene therapy. These medicaments, or genes identified by CC controlling a physiological or disease state (especially osteoporosis or controlling a physiological or disease state (especially osteoporosis or controlling a physiological or disease state (especially osteoporosis or controlling a physiological or disease state (especially osteoporosis or controlling a physiological or disease state (especially osteoporosis or controlling a physiological or controlling a controlling a physiologic bone density or other factors causing or contributing to osteoporosis its symptoms or other conditions involved in mechanical stress or its lack. The methods can also be used for advancing research or studies 'n 9 6

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Best Local 9
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08-AUG-1989;
28-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mega:karyocyte colony stimulating factor protein - regulates human haematopoiesis by stimulating growth and development of mega:karyocyte(s) in treatment of e.g. plastic anaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library. The sequence can be inserted into expression verthe prodon, of recombinant meg-CSF. The protein is used bleeding disorders and platelet deficiencies. See also AAR11372, AAR10870 and AAR10871.
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library. The sequence can be inserted into expression vectors
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                                                                                                                                                                             Tuberculosis; mycobacteria; infection; diagnosis;
antimycobacterial; antibiotic; vaccine.
                                                                                                                                                                                                                                                      AAW31852;
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N-PSDB; AAT93610.
                                                                                                                                                          Mycobacterium
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Pred. No. 1.2e-35;
3; Mismatches 6;
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                                                                                         Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma
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Matches 314
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fips. wipo.int/pub/published_pct_sequences.
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21-SEP-2000;
27-SEP-2000;
384 kttsssaestehgertplanenttpspaeptenrertanenttpspagptenrettanek
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30-JUN-2000;
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                     Multimer; enzyme; complex; protein-protein interaction; dockerin domain; cohesin domain; catalytic subunit; scaffold subunit; SdbA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.
                                                                                                                        C. thermocellum OlpB protein
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                                                                                                                                                                                                                                                                                        ppptttlppssptsppnnspsppppksqpppppprfqppppprgtcp
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990S-0161406
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99US-0161359
99US-0161360
99US-0161361
99US-0161920
99US-0161992
99US-0161993
99US-0161993
   Location/Qualifiers
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                                                                                                                                                                                                                  Protein; 1664 AA
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Pred. No. 1.2e-47;
4; Mismatches 293;
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by protein protein, especially enzymatic, complexes are held together conditions and cohesins, which are found on the catalytic and scaffold subunits and cohesins, which are found on the catalytic and scaffold subunits respectively. An example of such a complex is the cellulose degrading protein complex from Clostridium thermocellum, known as the cellulosome. This complex comprises around 15 proteins including endoglucanases, cellubiohydratases, hemicallulases, e.g. xylanases or lichinases, which cellulosome integrating protein (CipA; see AAWA3108). The catalytic subunits of domains. Cip has been shown to contain 9 copies of a cohesin domain. Compains Cip has been shown to contain 9 copies of a cohesin domain. The invention relates to the isolation of proteins binding to a novel dockerin type domain found in the C-terminal portion of Cip. The new compains is designated a type II dockerin domain (Cip and the catalytic subunits of the cellulosome). The type Cip domain is designated a type II dockerin domain so compared to the type Cip but is unable to bind type I cohesin domains. The cellulosome of the olips gene. The sequence presented here is an example of a protein which binds the novel type II dockerin domains in the N-terminal portion of Cip. The new compains to the first domain (amino acid residues 28-192) is thought to hind the first domain (amino acid residues 28-192) is thought to complexes, especially enzyme complexes, to potentiate their catalytic complexes.
Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellulase proteins with cohesin or dockerin type II domains - useful for potentiating the activity of multiprotein enzyme complexes
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                                         actions in a synergistic manner.
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Query Match
Best Local Similarity 13.0%; 31.0%;

Length 1664;

Sequence

Ωy В QΥ 밁 Qy Matches 758 284 VLAKPTP-KAETTIKGPALTIPKEPIPTTPKEPASTIPKEPIPTTIKSAPTTPKEPAPTI 342 312; sdeptpsdeptps--deptps--deptp-sdeptpsetpeepiptdtpsdeptpsdeptp 919 КРАРТТРКЕРАРТТРКЕРТРТТРКЕРАРТТКЕРАРТ-ТРКЕРАРТАРККРАРТТРКЕРАР 457 eptpsetpeepiptdtpsdeptpsdeptpsdeptpsdeptpsdeptpsetpeepiptdtp 864 vviqpapikaasdepiptdtpsdeptps Conservative 104; Mismatches Score 950; DB 19; Pred. No. 1.6e-45; N4; Mismatches 361; --deptps---deptpsdeptpsd Indels 230; Gaps 804

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16-APR 1999
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23-APR 1999
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29-MAR-1999;
01-APR-1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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hybridisation assay; genetic mapping; gene expression control;
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08-APR-1999;
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990S 0130077
990S 01300449.
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990S 0132048.
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99US-0128234.
99US-0128714.
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99US-0123548.
99US-0125788.
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99US-0126785
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promoter;
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The invention relates to a method of treating osteoarthritis via the CR administration of a composition comprising the camptodactyly-arthropathy-CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. CC The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous in the invention may be administered via intra-articular or intravenous being megakaryocyte stimulating factor (MSF). The gene encoding CC CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-CC arthropathy-coxa vara-pericarditis, in which patients have synovial CC hyperplasia without evidence of inflammation. CACP protein (MSF) cacts as a synovium lubricant, and can be used to lubricate tissue and CC applied to reduce the symptoms of osteoarthritis. The composition may be composed to reduce the symptoms of osteoarthritis (e.g., joint pain, CC represents the bovine orthologue of human MSF, superficial zone
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                           1143
                                                                                                                                                                                                                           1023
                                                                                                                                                            1083
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                  964 PKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRK-MTSTMPELNPT 1022
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                            Local Sin
hes 319;
                                                                                                            ALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEWTQVRRRRFE
                                             s-lpeamlqtttrptptpnseildvnsenedgdaaegekphmifrppvltpivipgteii
                                                                                                                                                                                                    SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL 1082
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                                                                                                                                                                                                                                                                                                                          Conservative
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2000US-0145328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tein; camptodactyly-arthropathy-coxa vara-pericarditis;
protein; 32P; MSF orthologue; synovial lubricant;
                                                                                                                                                                                                                                                                                                                     23.3%; Score 1707.5; DB 22; 79.9%; Pred. No. 6.7e-89; tive 24; Mismatches 53; ]
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                                                                                                                                                                                                                                                                                                                                                     Length
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The present invention describes coion cumour associated process of the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (CII) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) (CII) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) (CII) may be used to treat disorders associated with decreased expression by activity of TCAPs by expressing inactive proteins or to supplement the CII patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences in the production assays to detect and complementary sequences in the production assays to detect and complementary sequences in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used to down regulate complementary and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples.
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10-JAN-2000; 2000US-05480331.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-059448.
28-AUG-2000; 2000US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes colon tumour associated proteins (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colon tumor associated proteins and nucleic acids useful prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immunotherapy; diagnosis; colon cancer; colon tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                               2; Page 446-462; 472pp; English.
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E, Wang T,
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vetkettttnkqtstdgkekttsaketqsiektsakdlaptskvlakptpkaetttkgpa

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Best Local 9
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                                                                                                                                                                                                                                                                                                                              This sequence represents the human megakaryocytopoientin (MPO) protein. This sequence was purified using a carrier which can couple wheat germ agglutinin and heparin to separate MPO. Fragments of this sequence (see AAR80039 and AAR80040) were used to produce the amplification primers shown in AAT04544 and AAT04545. The fragments amplified by these primers can then be used as probes to screen human cDNA libraries for MPO cDNA. The MPO cDNA can then be inserted into a plasmid which is used to transform cells to produce MPO. The MPO sequence is capable of promoting colony formation of megakaryocytes, enlarging the size of megakaryocytes and stimulating the proliferation of multipotential stem cells. The factor may be used for treating thrombocytopenia and hematocytopenia.
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                                                                                                                                                                                                                                                                                     The purification method can be used to isolate MPO from human urine or serums of patients with aplastic anaemia, and from animal blood or urine by radiation exposing the animals to induce aplastic anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 23; 36pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombocytopenia
                                                                                                                                                                                                                                                             Sequence
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DB; AAT04546.
KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 120
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Pred. No. 2.5e-118;
3; Mismatches 21; 1
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RESULT
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ID AAB6
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AC AAB6
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DT 27-A
27-APR-2001
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                                standard;
(first entry)
                                Protein;
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PKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKE 454 papttpkepaptttkepaptttkshpplprscxxxxctqp

361 361

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  23-APR-1999;
                    24-APR-2000;
                                                          WO200064930-A2
                                                                                 Homo
                                                                                                             numan tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy.
                                                                                                                                                                                                                       AAB29778 standard; Protein;
                                                                                                    osteopathic.
                                                                                                                                         Human tribonectin; MSF;
                                                                                                                                                             Human MSF-derived tribonectin.
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47.6%; Score 3484; 74.6%; Pred. No. 7

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The invention relates to a human tribonectin which is a product of calternative splicing of the human MSF (megakaryocyte stimulating factor) compensation of the human MSF (megakaryocyte stimulating factor) compensation of a motify and has a polypeptide sequence comprising 1-76 compensation of a motify having at least 50% identity to the sequence KEPAPTT human MSF-derived tribonectin; a blocompatible composition comprising a company of the invention also relates to a nucleic acid encoding a computation of the invention also relates to a nucleic acid encoding a computation; and a method measuring the amount of MSF or its fragment in a biological sample of a company of the amount of MSF or its fragment in a biological sample of a control company of the presence of or predisposition to developing costeoarthritis. The tribonectin and DNA encoding it are useful in the content of osteoarthritis, where they may be used for lubricating content of the predisposition to developing content content in the content of content of the predisposition to developing content of content of osteoarthritis, where they may be used for lubricating content of the predisposition to developing content of the predisposition to developing content of content of osteoarthritis, where they may be used for lubricating content of the predisposition to developing control the predisposition to developing control content of the predisposition to developing control content of the predisposition to developing control content of the predi
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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating molety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a
                                                                                Claim
                                                                                            Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; MSF; megakaryocyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human megakaryocyte stimulating factor (MSF,
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                                                                                                                                                                                            The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis (CACC) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous injection. The human CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-arthropathy-coxa vara-pericarditis, in which pattents have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) acts as a synovium lubricant, and can be used to lubricate tissue and acts as a synovium lubricant, and can be used to lubricate tissue and applied to reduce the symptoms of osteoarthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthrities (e.g., joint pain, applied to reduce the symptoms of osteoarthrities and the symptoms of osteoarthrities and the symptoms of osteoarthrit
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                                                    applied to reduce the symptoms of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence represents human megakaryocyte stimulating factor (MSF, CACP protein). Note: This sequence is not given in its entirety in figure 4 of the specification, although a GenBank accession number was given. This sequence was therefore obtained from GenBank (U70316).
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TKTPAATKPEMTTTAKOKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV
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96.9%;
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Pred. No. 0;
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CC stimulating factor (MSF) precursor. The sequence covered by exons II, CC sequence is modified by the addition of an N-terminal sequence encoding CC a secretory leader, an initiating methionine proceeding sequence sequences derived from human megakarycety colony stimulating factor (MSF). This CC asequences derived from human megakarycety colony stimulating factor (MSF). Exon I contains the initiating methionine, and encodes a CC encoding the original meg-CSF includes exons II-TV and is thought to classical mammalian protein secretion signal sequence. The sequence cc encoding the original meg-CSF includes exons II-TV and is thought to classical family of mRNA's each encoding a different ways to CC yield a family of mRNA's each encoding a different ways to CC yield a family of mRNA's each encoding a different ways to CC wand VI are thought to be related to the activity of the factor and CC are also implicated in the stability, folding and processing of the CC synergy of MSF with other cytokines. Exons V - XII are believed to be claimed in the processing or folding of the appropriate structure of CC implicated in the processing or folding of the appropriate structure of CC sequences which direct proteolytic cleavage, adhesion, organisation of CC the cellular matrix or extracellular matrix processing. Both naturally occuring and non-naturally occuring MSF's may be characterised by with the exons spliced together in differing orders to form different tips of the members of the MSF family.
       Query
Best L
                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence given stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human mega-karyocyte stimulating factors - for immune deficiencies, cancer, exposure to radiation bacterial and viral infections, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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10-SEP-1991;
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Local Similarity
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DB; AAQ27223.
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91US-0757022.
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1331..1373
/label= Exon_XI
1373..1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is a full length translation from the megakaryocyte (MSF) precursor. The sequence covered by exons II, megakaryocyte stimulating factor (MSF). This
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Conservative
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                                                                                     Score 7291.5;
Pred. No. 0;
0; Mismatches
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tktpaatkpemtttakdktterdlrttpetttaapkmtketatttektteskitatttqv
                                                                                                                                                  TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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No.
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1: /SIDSB/gcgdata
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                       7291.5
7291.5
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                                                                                                                                                                                                                                                                                                                                                                             Match
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                                                                                                             This novel 55 kDa protein is encoded by an open reading frame of a Mycobacterium tuberulosis DNA fragment (see AAM93610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAM93851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4258
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antimycobacterial; antibiotic;
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                                                                                                                                                                                                                                                                            Claim 11; Fig 16; 55pp; English.
                                                                                                                                                                                                                                                                                                                  New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring
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The present sequence is obtained from a clustral x alignment with CC protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the CC 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the CC identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular fractions and extracting mRNA from them, and differentially analysing the genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
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                                               Probe; human; breast disease; breast inflammatory disease; proliferative b
 WO200157270-A2
                                                                                    Peptide #2327 encoded by probe for measuring
                          Homo sapiens
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Best Local Similarity
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fips. Wipo.int/pub/published_pct_sequences.
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                           TP----TTPKEPAPT-TKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPA---PTT 417
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                                                                                                                                            TPKEPASTTPKEPTPTTIKSA--PTTPKEPAPT-----TTKSAPTTPKEPAPTTTK 309
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human breast -
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2000US-0236359.
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Pred. No. 5.8e-37;
9; Mismatches 492;
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Matches 226;
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25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                        Multimer; enzyme; complex; protein-protein interaction; dockerin domain; cohesin domain; catalytic subunit; scaffold subunit; SdbA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.
                                                                                                                         C. thermocellum OlpB protein.
                                                                                                                                                                                   AAW43106
                                                                                                                                                                                                                 AAW43106 standard;
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                                                                                                                                                      16-OCT-1998
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                                Clostridium
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                                thermocellum
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99US-0161406
99US-0161406
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99US-0161360
99US-0161361
99US-0161920
99US-0161992
99US-0161993
99US-0161993
   Location/Qualifiers
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Pred. No. 4.4e
24; Mismatches
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Aw Multimeric protein, especially enzymatic, complexes are held together CC by protein-protein interactions between domains designated dockerins CC and cohesins, which are found on the catalytic and scaffold subunits CC and cohesins, which are found on the catalytic and scaffold subunits CC protein complex from Clostridium thermocellum, known as the celluloscome. CC chis complex comprises around 15 proteins including endoglucanases, cc cellobiohydratases, hemicellulases, e.g. xylanases or lichinases, which cintegrating protein (CipA; see AAW43108). The catalytic subunits CC integrating protein (CipA; see AAW43108). The catalytic subunits CC integrating protein (CipA; see AAW43108). The catalytic subunits CC domains. Cip has been shown to contain 9 copies of a cohesin domain. CC dockerin type domain found in the C-terminal portion of Cip. The new CC domain is designated a type II dockerin domain (as compared to the type CC I dockerin domain found on the catalytic subunits of the cellulosome). The type CC I dockerin domain has some sequence similarity to the type I dockerins but is unable to bind type I cohesin domains. CC the novel type II dockerin and is the product of the OlpB gene. CC the protein contains 4 type II cohesin domains in the N-terminal portion of which the first domain (amino acid residues 28-92) is thought to bind CipA. The novel type II dockerin and cohesin domains can be used to bind CipA. The novel type II dockerin and cohesin domains can be used in complexes. especially enzyme complexes, to potentiate their catalytic catalytic contains 4 type II dockerin and cohesin domains can be used to bind CipA. The novel type II dockerin and cohesin domains can be used to bind CipA. The novel type Complexes.
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N-PSDB; AAT86623.
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                                        actions in a synergistic manner.
  Sequence
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Matches 312; Conserv
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sdeptpsdeptps--deptps--deptp-sdeptpsetpeepiptdtpsdeptpsdeptp
                  KPAPTTPKEPAPTTPKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 407
                                                              \verb"eptpsetpeepiptdtpsdeptpsdeptpsdeptpsdeptpsetpeepiptdtp" \\
                                                                                              TKSAPTTPKEPAPTTTKEPAPTTPKEPA----PTTTKEPAPTTTKSAPTTPKEPAPTTPK 348
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                                                                                                                                                                                                   Conservative 104;
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Pred. No. 6.6e-47;
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9905-0144814 9905-0145086 9905-0145088 9905-0145085 9905-0145087 9905-0145089 9905-0145192 9905-0145195 9905-0145145 9905-0145218	99US-0144085. 99US-0144086. 99US-0144325. 99US-0144331. 99US-0144333. 99US-0144333. 99US-0144333. 99US-0144335. 99US-0144352. 99US-0144352.	990S-013983 990S-013989 990S-0140353 990S-0140554 990S-0140695 990S-0141287 990S-0141287 990S-0141287 990S-014254 990S-014205 990S-014292 990S-014292 990S-014292 990S-014292 990S-014292 990S-014292 990S-014292 990S-014292	990S-013476 990S-013476 990S-013476 990S-0135124 990S-013535 990S-0135629 990S-0135782 990S-0135782 990S-0137528 990S-0137528 990S-0137528 990S-0137528 990S-0137528 990S-0139454 990S-0139453 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139458 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139459 990S-0139459 990S-0139459 990S-0139459 990S-0139459 990S-0139459 990S-0139460 990S-0139460 990S-0139460 990S-0139460
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14-OCT-1999; 99US-01596; 18-OCT-1999; 99US-016072 21-OCT-1999; 99US-016072 21-OCT-1999; 99US-016072 21-OCT-1999; 99US-016073 21-OCT-1999; 99US-016081 21-OCT-1999; 99US-016081 21-OCT-1999; 99US-016081 22-OCT-1999; 99US-016081 22-OCT-1999; 99US-016081 22-OCT-1999; 99US-016098 22-OCT-1999; 99US-016098	06-OCT-1999; 99US-01578 07-OCT-1999; 99US-01580; 08-OCT-1999; 99US-01583; 12-OCT-1999; 99US-01583; 13-OCT-1999; 99US-01592; 13-OCT-1999; 99US-01592; 13-OCT-1999; 99US-01592; 14-OCT-1999; 99US-01593; 14-OCT-1999; 99US-01593; 14-OCT-1999; 99US-01593; 14-OCT-1999; 99US-01593;	7-AUG-1999; 99US-01510 27-AUG-1999; 99US-01513 30-AUG-1999; 99US-01513 31-AUG-1999; 99US-01513 31-AUG-1999; 99US-01513 31-AUG-1999; 99US-01530 07-SEP-1999; 99US-01530 10-SEP-1999; 99US-01530 13-SEP-1999; 99US-01540 20-SEP-1999; 99US-01540 20-SEP-1999; 99US-01554 23-SEP-1999; 99US-01554 24-SEP-1999; 99US-01554 24-SEP-1999; 99US-01554 29-SEP-1999; 99US-01554 29-SEP-1999; 99US-01555 04-OCT-1999; 99US-01565 04-OCT-1999; 99US-01571	26-JUL- 27-JUL- 27-JUL- 27-JUL- 28-JUG- 02-AUG- 02-AUG- 02-AUG- 02-AUG- 03-AUG- 03-AUG- 05-AUG- 05-AUG- 05-AUG- 11-AUG

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Protein identification; hybridisation assay; ger Arabidopsis thaliana Arabidopsis thaliana termination sequence genetic protein signal transduction pathway; metabolic
netic mapping; gene expression control; fragment SEQ ID NO: 48115

promoter; pathway;

RESULT
AAG3892
ID AAG38
XX AAG38
AC AAG3
XX AAG38
AC AAG3
XX Prot
XX Prot
XX Prot
XX EP10
XX E 08-APR-1999; 16-APR-1999; 19-APR-1999; 21-APR-1999; 23-APR-1999; 23-APR-1999; 28-APR-1999; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; 01-APR-1999; 06-APR-1999; 30-APR-1999; 30-APR-1999; 04-MAY-1999; 05-MAY-1999; 06-MAY-1999; 06-MAY-1999; 07-MAY-1999; 11-MAY-1999; 14-MAY-1999; 25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 25-FEB-2000; 06-SEP-2000 EP1033405-A2 2000EP-0301439 99US-0126785. 99US-0127462. 99US-0128234. 99US-0128714. 99US-0129845. 99US-0132407. 99US-0132484. 99US-0132486. 99US-0132486. 99US-0132487. 99US-0132863. 99US-0134256. 99US-0134218. - 2066 - 5066 - 5066 - 5066 - 5066 - 5066 - 5066 99US-0123548 99US-0125788 99US-0121825 99US-0123180 s-0126264. s-0126785. 3-0130891. 3-0131449. -0130077. -0130449. -0132048. -0132407. 0130510

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cc administration of a composition comprising the camptodactyly arthropathy-
cc coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.
CC The composition may further comprise a local anaesthetic. The composition
CC of the invention may be administered via intra-articular or intravenous
CC injection. The human CACP protein is identified in the invention as
CC being megakaryocyte stimulating factor (MSF). The gene encoding
CC CACP protein (MSF) is located on chromosome 1925-31, and mutations in
CC this gene are responsible for the heritable disorder camptodactyly-
CC arthropathy-coxa vara-pericarditis, in which patients have synovial
CC hyperplasia without evidence of inflammation. CACP protein (MSF)
CC acts as a synovium lubricant, and can be used to lubricate tissue and
CC joints in the treatment of osteoarthritis. The composition may be
CC applied to reduce the symptoms of osteoarthritis (e.g., joint-pain,
CC loss of range of movement or joint damage). The present sequence
CC represents the bovine orthologue of human MSF, superficial zone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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les 319; Conserv
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79.9%; Pred. No. 2e-91;
tive 24; Mismatches
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10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 446-462; 472pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevention,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer.
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2000US-0519444.
2000US-0575251.
2000US-0609448.
2000US-0649811.
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Jiang Y;
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paptt-kepaptt-kepaptt-kepaptt-kepaptt-kepap-----ttk

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                                                                                                                                                      megakaryocyte;
multipotential
                                                                                                                                                                    Human; megakaryocytopoientin; wheat germ agglutinin;
(SHAN-) SHANGHAI BEITI BIOTECHNOLOGY CO
                 04-MAR-1994;
                                  06-MAR-1995;
                                                                                             Misc-difference
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                                                                                                                                                      aplastic anaemia; thrombocytopenia; stem cell.
                 94CN-0112066
                                  95WO-CN00015
                                                                                                            Location/Qualifiers 393..396
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RESULT AAB60569

Protein;

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27-APR-2001 AAB60569;

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Best Local :
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                                                                                                                                                                                                                                                                                              ppsgasqtiksttkrspkppnkkktkkvieseeitevkdnkknrtkkkptpkppvvdeag
                                                                         PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTT
                                                                                                                  {\tt lttpkeptpttpkepasttpkeptpttiksapttpkepaptttksapttpkepaptttke}
                                                                                                                                                                             SGLDNGDEKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT
prslhpptkepapttpkepaptapkkpaplpple
                             PKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKE 404
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3; Mismatches 21;
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RESULT
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                                                                                             Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic;
                24-APR-2000; 2000WO-US10953
                                   02-NOV-2000
                                                     WO200064930-A2
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9908-0298970
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Query Match Best Local S Matches 794

Local Similarity wes 794; Conserv

Conservative

28;

Score 3484; DB 22; Pred. No. 4.9e-194; 8; Mismatches 80;

Indels Length

162;

Gaps

66;

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The invention relates to a human tribonectin which is a product of CC alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide CC lubricating molety and has a polypeptide sequence comprising 1-76 CC (AAB29774). The invention also relates to a nucleic acid encoding a CC human MSF-derived tribonectin; a blocompatible composition comprising a CC human MSF-derived tribonectin; a blocompatible composition comprising a CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by CC measuring the amount of MSF or its fragment in a biological sample of a CC indicates the presence of or predisposition to developing CC osteoarthritis. The tribonectin and DNA encoding it are useful in the CC treatment of osteoarthritis, where they may be used for lubricating CC mammalian joints, such as articulating joints of humans, dogs or horses. CT he tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured CC insues of a mammal, where the injury is caused by a surgical insertion CC rationar, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents cc a substantial portion of a human MSF-derived tribonectin.
Sequence
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                                                                                        Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque;
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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor: gene. The tribonectin has at least one O-linked oligosaccharide lubricating modety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEDAPTT (AAB29774). The invention also relates to a nucleic acid encoding a
                                                                                                                                                                                                                         Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety
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CC human MSF-derived tribonectin; a biocompatible composition comprising a CC human tribonectin for inhibiting tissue adhesion formation; and a method of diagnosing osteoarthritis or a predisposition to osteoarthritis by CC measuring the amount of MSF or its fragment in a biological sample of a cindicates the presence of or predisposition to developing control con
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                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camprodactyly-arthropathy-coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous injection. The human CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-arthropathy.
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                                                                      applied to reduce the symptoms of osteoarthritis (e.g., joint pain, applied to reduce the symptoms of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence represents human megakaryocyte stimulating factor (MSF, CACP protein). Note: This sequence is not given in its entirety in figure 4 of the specification, although a GenBank accession number was given. This sequence was therefore obtained from GenBank (U70316).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page -; 34pp; English.
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200107068-A1
                                                                                                                                                                                                                                                                        arthropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) acts as a synovium lubricant, and can be used to lubricate tissue ar joints in the treatment of osteoarthritis. The composition may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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2000US-0145328.
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Sequence

1404 AA

MRICHES 1311: CONSEIVATIVE 93.4% Pred. NO. 0; MISMETCHS 1311: CONSEIVATIVE 93: 0 MISMETCHS 0 MICHORS 1311: CONSEIVATIVE 93: 0 MISMETCHS 0 MISMETCHS 0 MISMETCHS 1311: CONSEIVATIVE 0 MISMETCHS 1311: CONSEIVATIVE 1311: CONSEI
hes 3311; Conservative 93.4%; Pred. No. 0; Indels 93 hes 3311; Conservative 97 Mismatches 97 hes 3312; Conservative 97 Mismatches 97 14 MarkTlpIy11111syrViQqVssqdlsscagrcgegysrdatcncdyncdynmocl 11 Mismatches

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В
                                                                                                                                                                                                                                                                                                                                                                       The sequence given is a full length translation from the megakaryocyte cc stimulating factor (MSF) precursor. The sequence covered by exons II, CC sequence is modified by the addition of an N-terminal sequence encoding cc terminating codon following exon IV. The cDNA sequence given contains cc (meg-CSF). Exon I contains the initiating methionine, and encodes a cc encoding the original meg-CSF includes exons II-IV and is thought to colony stimulating factor cc classical mammalian protein secretion signal sequence. The sequence cc encoding the original meg-CSF includes exons II-IV and is thought to classical mammalian protein secretion signal sequence. The sequence cc yield a family of mRNA's each encoding a different ways to primary transcript of this gene may be cleaved in different ways to cc y and VI are thought to be related to the activity of the factor and cc are also implicated in the stability, folding and processing of the synegy of MSF with other cytokines. Exons V - XII are believed to be completed in the processing or folding of the appropriate structure of the cellular matrix or extracellular matrix processing. Both naturally cccuring and non-naturally occuring MSF's may be characterised by with the exons spliced together in different to form different combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different combinations of alternatively spliced exons from this sequence, which different in differing orders to form different combinations of alternatively spliced exons from this sequence, which matrix processing to the sequence in the exons spliced together in differing orders to form different combinations of alternatively spliced exons from this sequence, which the exons spliced together in differing orders to form different combinations of alternatively spliced exons to form this sequence.
                                                                                                                                                                                                                                 Query Match 99.2
Best Local Similarity 93.4
Matches 1311; Conservative
                                                                                                                                                                                                                                                                                                                                      Sequence
121 ppsgasqtiksttkrspkppnkkktkkvieseeiteehsvsenqessssssssssssstiw 180
                                                    107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human mega-karyocyte stimulating factors - for treating immune deficiencies, cancer, exposure to radiation or drugs bacterial and viral infections, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-1991;
10-SEP-1991;
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                                                                    (GEMY ) GENETICS INST INC.
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91US-0757022
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1373..1404
/label= Exon_XII
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/label= Exon_X
1331..1373
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0; Mismatches
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167	RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY 11 	108 201	Оy
107 200	INLENGKPVIGETTERNOTEVAFRGHYFWMESPESPPSPARRITEVWGIPSPIDTVFT		Db 42
140	TENSKLVEVENEKSEDAGGAEGETPHMLLRPHYEMPEVTPDMDYLPRVPNOGIIINPMLS 1	081	P 5
87 080	CKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN 9 	21	B &
020	STITEDITERKITILAPKVTTTKKTITTEIMNKPEETAKPKDRATNSKATTPK 9		B 5
60	AIPAAIKPEMUTTAKOKTTEBOLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV 8		} B \$
307	APTIPETPPTISEVSIPTIKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 8	841	g
340	APILIKEPAPTTPKAKPAKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK 7	781) B 4
587		721	D
ี ผู้	PUTTRKKADARNTEKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP	661	04 p 45
56 7 660		601	? B &
507	- A SAKII KAESPITIKEPAPITPKEPAPTTPKKPAPTTPKEPAPTTPKKP 	541	S B 7
	"PKAPPAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 	481 481	2 B 2
387 480	TITASAPTIPKEPAPTTPKEPAPTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPK 	421) B (
327 420	TPREPTPTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKEP	361 379	2 B 6
26 7 360	KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS 	208 301	Qy Db
20 7 300	TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTINKQTSTDG 	148 241	Db Qy
147 240	kikssknsaanreiqkkikvkdnkknrtkkk		dd Vo

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Scoring table:
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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2: /SIDS8/gcgdata,
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7064
1 MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1311
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Gapop 10.0 ,
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99.2
99.2
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MSF precursor. Sy Human megakaryocyt Human megakaryocyt Human EST encoded Human MSF-derived Human MSF-ortholo C899P predicted am Arabidopsis thalia C. thermocellum Ol peptide #2327 enco
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i.		21	1610	6.1	429	44
Human O/Coz/ gene		22	2819	6.2	437.5	43
277777	AAR80839	16	751		442.5	42
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albican		20	750	6.5	456.5	7
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Human pro		22	1127		485	32
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Cycle predicted am		22	957		488	30
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e #286		22	617	6.9	488	28
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11 SSP2		13	826		488.5	26
ETON OT CTAP		21	1721		489	25
Human SKCAF. HOMO	AAB50362	22	3118		489.5	24
SRCAP.	AAB50363	22	2972	6.9	489.5	23
OKEX OKE	AAB41231	21	2971	7.0	496.5	22
30.	AAR26050		111	7.0	498	21
Œ	AAP82975	9	744	7.2	506.5	20
۲	AAB11726		1837	7.2		19
Amino acid sequenc	AAY54466		788	7.4	520.5	18
Protein encoded by	AAR10872		182	7.5	529	17
Amini acid sequenc	AAY54467	21	807	7.7		9 (
e or	AAP60570	7	844		547 5	7 .
-	AAW31855	18	572	8.7	612	14
Sequence 91/101/42	AAY53666	21	4412	8	627	<u>ω</u> :
Mycobacterium tube	AAW31852	18	763	10.1	715	7.2
Mycobacterium tube	9	0	1	,	1	

ALIGNMENTS

RESULT AAR26049

Region Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing. 02-FEB-1993 (first entry) AAR26049; AAR26049 standard; Protein; 1404 Region Region Region Key Synthetic. MSF precursor Region Region Region Region Region /label- Exon_II 67..107 /label= Exon_I 26..67 Location/Qualifiers 1166./label= Exon_III 107..157 /label= Exon_VIII 200 /label= /label= 'label= Exon_V 'label= Exon_IV 'label= Exon_VII pel= Exon_VI l..1166 .1141 . 200 .1212 .1266 Exon_IX AA

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Best Local S
Matches 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA and FIRA have antigenicity suitable for providing protective immunity against Plasmodium falciparum malarial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-1984;
11-SEP-1984;
10-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA coding for Plasmodium falciparum antigens - expressing poly:peptide(s) having antigenicity of RESA or FIRA antigens of
                                                                                                 336
                                                                                                                          497
                                                                                                                                                   285
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N-PSDB; AAN60473.
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                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 7.6%;
Local Similarity 25.7%;
hes 252; Conservative 128
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EKLAPTTPEKPAPTTPEELAPTTPEEPAPTTPKAAAPNTPKEPA----PTTP 644
                                      lesvkqnadeqkeqptdsqisvnaqdsvtiqeptatqep-pttqelta----
                                                               PTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTP
                                                                                         vtveehidekkgsegdnislsslseeteekshtkkkksswlkfgrgnkndkksknekkps
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128; Mismatches 358;
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This novel 55 kDa protein is encoded by an open reading frame of a Mycobacterium tuberrulosis DNA fragment (see AAT95610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAW31851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis
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antimycobacterial; antibiotic;
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                                                                                                                                                                                       New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
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The present sequence is obtained from a clustral x alignment with protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the
                                                                                                                    Claim 32; Fig 6A-R; 308pp; English
                                                                                                                                                                          Identification of stress induced preventing, treating or controlli
                                                                                                                                                                                                                                                                   WPI; 2000-053304/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis; mycobacteria;
antimycobacterial; antibioti
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development,
                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                 inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                  Novel single exon in a human breast
                                                                                                                                                                                                                                                                         WPI; 2001-476286/51.
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30-JUN-2000;
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                        ftp.wipo.int/pub/published_pct_sequences
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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Qy В δÃ ₽ Matches 106 272 244 212 156 148 Local Sin 88 51 35 spaeptenrerta---nenttlspaeptenrertanentapfpagptenremtanenttl tgtpeesektedsrttvasdklltkttkniqetisaneltqslaeptehggrtanenntp T-TPDTSTTQHNKVST--SPKITTAKPINPRPSLPPN----SDTSKETSLTVNKETTV ktgrpleksmstldktstsshktttsfhnsgnsqtkqkstsfpekitaa----skttykt AANRELQKKLKVKD---irn--qrsvdpadsttthk----esagkkhitpapkskincrksttgkstv----trksd eiheqkrhcnttrhskptdk--ptgnsktidhks---stdnheapptseenssnqgkdpm 105 ESFERGRECDCDAQCKKYDKCCP-----DYESFCAEVHNPTSPPSSKKAPPPSGASQT IKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSSTIWKIKSSKNS Conservative 122; Score 805; DB 22; pred. No. 3.1e-36; 2; Mismatches 517 -NKKNRTKKKPTPKPPVVDEAGSGLDNGDFKV 517; Indels Gaps 192 155 147 87 328 243 211 285 271 47;

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Query Match Best Local

Similarity

11.1%; 26.2%;

Length 1325;

Sequence

1325 AA;

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25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
C. thermocellum OlpB protein
                           16-OCT-1998
                                                     AAW43106;
                                                                             AAW43106 standard;
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28-OCT-1999;
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99US-0161405
99US-0161359
99US-0161359
99US-0161360
99US-0161361
99US-0161920
99US-0161992
99US-0161993
99US-0162142
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Pred. No. 3.9e-46;
4; Mismatches 293;
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Claim 7; Page 31-39; 60pp; French.
                                                                                                                                                                                                   Cellulase proteins with cohesin or dockerin type II domains - of potentiating the activity of multiprotein enzyme complexes
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                                                                                                                                                                                                                                                                         10-MAY-1996;
                                                                                                                                                                                                                                                                                                    14-NOV-1997.
                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                               Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                Multimer; enzyme; complex; protein-protein interaction; dockerin domain cohesin domain; catalytic subunit; scaffold subunit; SdbA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.
                                                                                                                                                                                                                                                                                      10-MAY-1996;
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207..3
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    useful
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Multimeric protein, especially enzymatic, complexes are held together CC by protein-protein interactions between domains designated dockerins CC and cohesins, which are found on the catalytic and scaffold subunits CC respectively. An example of such a complex is the cellulose degrading CC protein complex from Clostridium thermocellum, known as the cellulosome. CC This complex comprises around 15 proteins including endoglucanases, cellubiohydratases, hemicellulases, e.g. xylanases or lichinases, which CC interact with a central "scaffold" protein designated the cellulosome CC interact with the Cip subunit via conserved 23 amino acid dockerin CC interact with the Cip subunit via conserved 23 amino acid dockerin CC The invention relates to the isolation of proteins binding to a novel CC dockerin type domain found in the C-terminal portion of Cip. The new CC domain is designated a type II dockerin domain (as compared to the type CI I dockerin domain has some sequence similarity to the type II dockerin domain (as compared to the type CI I dockerin domain domain to the type II dockerin domains.

CC The sequence presented here is an example of a protein which binds CC The protein contains 4 type II cohesin domains in the N-terminal portion CC for which the first domain (amino acid residues 28-192) is thought to bind the first domain (amino acid residues 28-192) is thought to complexes, മ The novel type II dockerin and cohesin domains can be used s, especially enzyme complexes, to potentiate their catalytic a synergistic manner. synergistic

Sequence 1664 AA;

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                                     Qy
               758
                                      286 VLAKPTP-KAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTT 344
                                                              Local Si
hes 312;
|: :| | || :
vviqpapikaasdepiptdtpsdeptps-
                                                                          Similarity
                                                                       13.1%;
                                                              104;
                                                             Score 950; DB 19;
Pred. No. 4.4e-44;
4; Mismatches 361;
                                                                                    Length 1664;
                                                              Gaps
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30 - APR - 1999 04 - MAY - 1999 05 - MAY - 1999 06 - MAY - 1999 14 - MAY - 1999 18 - MAY - 1999 19 - MAY - 1999 10 - MAY - 1999 20 - MAY - 1999 21 - MAY - 1999 22 - MAY - 1999 23 - MAY - 1999 04 - JUN - 1999 06 - JUN - 1999 16 - JUN - 1999 16 - JUN - 1999 17 - JUN - 1999 18 - JUN - 1999 19 - JUL - 1999 10 - JUL - 1999 11 - JUL - 1999 11 - JUL - 1999 12 - JUL - 1999 13 - JUL - 1999 14 - JUL - 1999 15 - JUL - 1999 16 - JUL - 1999 17 - JUL - 1999 18 - JUL - 1999 18 - JUL - 1999 18 - JUL - 1999 19 - JUL - 1999 10 - JUL - 1999 11 - JUL - 1999 11 - JUL - 1999 12 - JUL - 1999 13 - JUL - 1999 14 - JUL - 1999 15 - JUL - 1999 16 - JUL - 1999 17 - JUL - 1999 18 - JUL - 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1081 scdtggdcecfcsavasyaqectkegacvfwrtpdlcp---ifc-dyynpphecewhyep
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                               \tt dvpigqlgqtvvcdvsvglicknedqkpggvipmafclnyeinvqccecvtqpttmtttt
                                                                                                  {\tt fspfstttpttpcvplcnwtgwldsgkpnfhkpggdteligdvcgpgwaaniscratmyp}
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29.3%;
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Pred. No. 7
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16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
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29-MAR-1999;
01-APR-1999;
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                                                                                                                                                                                                                                                                                          protein identification; signal transduction
hybridisation assay; genetic mapping; gene e
                                                                                                                                  09-MAR-1999;
23-MAR-1999;
                                                                                                                                                                                         25-FEB-2000;
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                                                                                                                                                                                                                                                          Arabidopsis thaliana
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 990S-0127462.
990S-0128234.
990S-0128714.
990S-0129845.
990S-0130077.
990S-0130049.
990S-0130510.
990S-0131449.
990S-0132048.
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99US-0126785
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promoter;
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                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of treating osteoarthritis via the Caddinistration of a composition comprising the camptodactyly-arthropathy-CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. CC The composition may further comprise a local anaesthetic The composition of the invention may be administered via intra-articular or intravenous in the chromatory of the stimulating factor (MSF). The gene encoding CC ching megakaryocyte stimulating factor (MSF). The gene encoding CC CACP protein (MSF) is located on chromosome 1q25-31, and mutations in CC this gene are responsible for the heritable disorder camptodactyly-CC arthropathy-coxa vara-pericarditis, in which patients have synovial CC hyperplasia without evidence of inflammation. CACP protein (MSF) CC acts as a synovium lubricant, and can be used to lubricate tissue and CC joints in the treatment of osteoarthritis. The composition may be CC applied to reduce the symptoms of osteoarthritis (e.g., joint pain, CC loss of range of movement or joint damage). The present sequence CC represents the bovine orthologue of human MSF, superficial zone
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 319; Conser
                                                                                            1085
                                                                                                                                                             1025
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                                                          194
                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising the camptodactyly-arthropathy-coxavara-pericarditis protein in combination with an anesthetic, user treating osteoarthritis, or as lubricants of tissue and joints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warman
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19-JUL-2000;
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TEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVA
                                                SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL 1084
                                                                                                                  s-lpeamlqtttrptptpnseiidvnsenedgdaaegekphmifrppvltpivipgteii 193
                                                                                                                                                                                    pkgratnsgvttpkpgkptkapkkptstkkprt-prvrkpkttptppktttsampeptpt 134
                                                                                                                                                                                                                                                                                                                                                                              (SZP).
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10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
                                                                                                                                                                 Claim 2; Page 446-462; 472pp; English.
                                                                                                                                                                                        prevention,
                                                                                                                                                                                                                   WPI; 2001-441847/47
                                                                                                                                                                                                                                      King
                                                                                                                                                                                                                                                Xu J,
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28-AUG-2000;
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                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenic;
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                                                                                                                                                                                    tumor associated proteins and nucleic acids useful for ntion, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          raigpsqvhtirihytpvrvpyqdkgflhnevkvstlwrglpnvvtsaislpnirkpdgy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted
                                                                                                                                                                                                                                    Lodes MJ,
E, Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy; diagnosis; colon cancer; colon tumour;
genic; gene therapy; vaccine; colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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2000US-05194629.
2000US-0519444.
2000US-0575251.
2000US-0609448.
2000US-0649811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid sequence
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                                                                                                                                                                                                                                     Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                              Benson
                                                                                                                                                                                                                                              DR,
                                                                                                                                                                                                                                             Meagher MJ,
                                                                                                                                                                                                                                            Stolk JA;
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The present invention describes colour cumports the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by crectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and therefore which patients may be in need of restorative therapy. (I) may be used as antigens in the production of antibodies against TCAPs

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multipotential
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 (SHAN-) SHANGHAI BEITI BIOTECHNOLOGY CO
                  04-MAR-1994;
                                  06-MAR-1995;
                                                  08-SEP-1995
                                                                   W09523861-A1
                                                                                           Misc-difference
                                                                                                           Misc-difference
                                                                                                                                                                   Human; megakaryocytopoientin;
                                                                                                                                                                                    Human megakaryocytopoientin
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                                                                                                                                                                                                    (first entry)
                                                                                                                                                 yvvyvopoientin; wheat germ agglutinin; heparin; aplastic anaemia; thrombocytopenia; hematocytostem cell.
                  94CN-0112066
                                  95WO-CN00015
                                                                                                          Location/Qualifiers 393..396
                                                                                            444..446
                                                                                                   /note=
                                                                                   /note=
                                                                                                   "unspecified
                                                                                  "unspecified
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                                                                                    amino acids'
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Matches 378
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DB; AAT04546.
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                                                                                     Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic;
                24-APR-2000;
                                 02-NOV-2000
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The invention relates to a human tribonectin which is a product of CC alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide CC lubricating moiety and has a polypeptide sequence comprising 1-76 CC (AAB29774). The invention also relates to a nucleic acid encoding a CC (AAB29774). The invention also relates to a nucleic acid encoding a CC human MSF-derived tribonectin; a blocompatible composition comprising a CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a condicates the presence of or predisposition to developing costeoarthritis. The tribonectin and DNA encoding it are useful in the CC mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is consected for inhibiting adhesion between two surfaces such as the injured CC or trauma, or an artificial device e.g., an orthopaedic implant. In comparity the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents a substantial portion of a human MSF-derived tribonectin.
Sequence
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밁 δõ Query Best I Matches 159 VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPIN y Match Local Sim hes 794; H Similarity Conservative 47.98; Score 3484; 1; Pred. No. 3.70 28; Mismatches ; DB 22; 3.7e-183; hes 80; Indels Length Gaps 218 60 66;

B Ş 망 δÃ 389 579 282 459 399 173 229 339 121 219 61 TPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKE 638 PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPT PKKPAPTTPKEPAPTTPKEPTTPKEPAPTTKEPAPTTPKEPAPTAPKKDAPTTPKEPA 458 paptt-kepaptt-kepaptt-kepap-ttkepaptt-kepaptt-kepapt ptt-kepap-ttkepaptt-kepapttkepap-ttkepaptt-kepap-ttke PTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE -kepaptt-kepaptt-kepaptt-kepaptt-kepaptt-kepaptt-kepa epaptttksapttpkepap-ttkepaptt-kepap-ttkepapttkepaptt-kepaptt EPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKSPAPTTTKSAPTTPKEPAPTT DLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEDASTTPKEPTPTTIKSAPTTPK ${\tt prpslppnsdtsketsltvnkettvetketttnkqtstdgkekitsaketqsiektsak}$ PRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK 278 vkdnkknrtkkkptpkppvvdeagsgldngdfkvttpdtsttqhnkvstspklttakpin388 578 335 398 172 120 281 228

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                                                                                         Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; tomato; monkey; dog; sea urchin; expressed sequence tag; ES diagnostics; forensic test; gene mapping; genetic disorder;
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17-JUL-2000;
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2000US-0617746
                       2001WO-US02687
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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating modety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a
                                                                                                                                                                                                       Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety
                                                                                                                                                                                                                                                                                                                 WPI;
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                        The invention relates to a method of treating osteoarthritis via the cadministration of a composition comprising the camptodactyly-arthropathy-
CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.
CC The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous composition. The human CACP protein is identified in the invention as composition to the invention as the protein (MSF) is located on chromosome 1925-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-cc arthropathy-coxa vara-pericarditis, in which patients have synovial cc acts as a synovium lubricant, and can be used to lubricate tissue and composition in the treatment of osteoarthritis. The composition may be completed to reduce the symptoms of osteoarthritis (e.g., joint pain, cc loss of range of movement or joint damage). The present sequence is not given in its entirety in figure 4 of the cc specification, although a GenBank accession number was given. This credit is contained from GenBank (U70316).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB60568 standard;
                                                                                                                                                                                                                                                                                                                                                                       New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, us treating osteoarthritis, or as lubricants of tissue and joints
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                           Example 1; Page -; 34pp; English.
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                                                                                                         TKTPAATKPENTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV
                                                                                                                                                                        \verb|kpapttpetpppttsevstptttkepttihkspdestpelsaeptpkalenspkepgvpt|
                                                                                                                                                                                            KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT
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tstttqdttpfkittlktttlapkvtttkktittteimnkpeetakpkdratnskattpk
                  TSTTTODTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK
                                                                                  {\tt tktpaatkpemtttakdktterdlrttpetttaapkmtketatttektteskitatttqv}
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The sequence given is a full length translation from the megakaryocyte CC III and IV encodes megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, compared by the addition of an N-terminal sequence encoding CC sequence is modified by the addition of an N-terminal sequence encoding CC a secretory leader, an initiating methionine proceeding exon II and a cc sequences derived from human megakaryocyte colony stimulating factor (MSF). Exon I contains the initiating methionine, and encodes a cc (meg-CSF). Exon I contains the initiating methionine, and encodes a concoding the original meg-CSF includes exons II-IV and is thought to terminate in the region between amino acid residues 134 - 147. The cc yield a family of mRNA's each encoding a different ways to V and VI are thought to be related to the activity of the factor and cc molecule. These exons are also thought to play a role in the observed implicated in the stability, folding and processing of the cc synergy of MSF with other cytokines. Exons V - XII are believed to be culting factor, ie. one or more of these exons may contain cc the resulting factor, ie. one or more of these exons may contain cc sequences which direct proteolytic cleavage, adhesion, organisation of cocuring and non-naturally occuring MSF's may be characterised by with the exons spliced together in differing orders to form different of the exons spliced together in differing orders to form different cc
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1, 2 and 3; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human mega-karyocyte stimulating fimmune deficiencies, cancer, exposure bacterial and viral infections, etc.
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10-SEP-1991;
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Ş S 밁 В 밁 Ş Ouery Match 99.6 Best Local Similarity 97.1 Matches 1363; Conservative 121 80 61 26 ppsgasqtiksttkrspkppnkkktkkvieseeiteehsvsengesssssssssssssstiw PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSSSTIW 139 ${\tt krvctaelsckgrcfesfergrecdcdaqckkydkccpdyesfcaevhnptsppsskkap}$ -----ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPESSKKAP 79 99.6%; Score 7245.5; Pred. No. 0; 0; Mismatches 0, DВ 0; 13; Indels Length 1404; 41; Gaps 180 ۲,

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DЪ Ş Вb Qy В Q В Ş B δÃ В ΩV 멍 δÃ В Ωy 망 Qγ В δÃ 밁 Š ₽ δÃ 밁 δÃ 1160 1141 1100 1081 1040 1021 980 961 920 098 901 841 800 781 740 721 680 661 601 560 541 500 481 440 421 380 361 320 301 260 241 200 181 140 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVET pqkptkapkkptstkkpktmprvrkpkttptprkmtstmpelnptsriaeamlqtttrpn POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELMPTSRIAEAMLQTTTRPN 1039 KPAPTTPETPPPTTSEVSTPTTTKEPTTTHKSPDESTPELSAEPTPKALENSPKEPGVPT kpapttpetpppttsevstptttkepttihkspdestpelsaeptpkalenspkepgvpt ${\tt tapttlkepapttpkkpapkelaptttkgptsttsdkpapttpketapttpkepapttpk}$ TAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK peepapttpkaaapntpkepapttpkepapttpkepapttpketapttpkgtapttlkep PEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP aptapkepapttpketapttpkkltpttpeklapttpekpapttpeelapttpeeptptt APTARKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPT 619 ttksapttpkepsptttkepapttpkepapttpkkpapttpkepapttpkepaptttkkp TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKP 559 aptttk sapttp kepapttp kkpapttp kepapttp keptpttp kepapttkepapttp kAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTPKEPAPTTPK ttpkeptpttlksapttpkepaptttksapttpkepaptttkepapttpkepaptttkep TTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEP 1080 1020 979 919 960 900 859 840 799 780 739 720 660 540 480 439 420 379 259

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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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7245.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAM24516
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AAW43106
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AAB60568
AAB29773
                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                 MSF precursor. Sy
Human megakaryocyt
Human EST encoded
Human MSF-derived
                                                                                                                                                                                                                                                    Description
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MSF precursor

Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing.

AAR26049 RESULT

AAR26049 standard; Protein; 1404 AA

AAR26049;

02-FEB-1993 (first entry)

AAB50362 AAR26042 AAR260487 AAM164587 AAM59288 AAM24513 AAB95541 AAB95541 AAB95541 AAB95541 AAB95541 AAM1483 AAM17406 AAM17406 AAM17406 AAR14160 AAR14160 AAR14161 AAR14161

Human MUC11 polype
C900P predicted am
Human protein sequ
Bioadhesive precur
peptide #1317 enco
peptide #1349 enco
peptide #1249 enco
Peptide #1289 enco
Human 07C027 gene
Human 07C027 gene

AAM14533 AAM26950 AAM02259

prp encoded by clo C. albicans Rbtl p Peptide #967 encod Peptide #987 encod Peptide #941 encod

PRP 378. Triticum Streptococcus pneu Human ORFX ORF2255

ALIGNMENTS

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AAR10872 AAP82975 L AAB11727 B AAW48299

AAB50363 AAB41231

Cryptosporidium pa Human ORFX ORF995 Human SRCAP. Homo Human SRCAP. Homo P. yoelli SSP2 ant Peptide #2892 enco Peptide #2899 enco

AAW31855 AAP60570

AAY53666

AAY54466 AAB11726

AAY54467

Sequence of the Fa Amini acid sequenc Amino acid sequenc Cryptosporidium pa Protein encoded by

Mycobacterium tube Sequence gi/101742 Mycobacterium tube

Bioadhesive precur Portion of Cryptos

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Human megakaryocyt Bovine MSF ortholo C899p predicted am Arabidopsis thalia C. thermocellum Ol

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Matches 248; Conserv
856 KTITTTEIMNKPEETAKPKDRATNSKATTPKPQK 889
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                                                                           MTKETATTTEKTTESKITATTTQVTSTTTQDTTPFK--ITTLKTTTLAPKVTT----TK 855
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26.6%; Pred. No. 6.2e-25;
ative 118; Mismatches 359;
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Db 811 epsttge--hadekkasegdnislsrlseeteek 842

Search completed: April 26, 2002, 16:24:52 Job time: 482 sec

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Best Local S
Matches 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculosis; mycobacteria; infection; diagnosis;
antimycobacterial; antibiotic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW31855 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
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                                                                                                                                                                                                                                                                    proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAW31851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 16; 55pp; English.
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Pred. No. 5.5e-29;
29; Mismatches 253
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11-SEP-1984;
10-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                         AAP60570;
                                                                                                                                                                                                                                                                                                                                                                                                                               AAP60570
The inventors claim nucleotide sequence
                                                                                                                                                                                                                                                      27-MAR-1986
                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
                                                                                                                                    Kemp DJ,
                                                                                                                                                                                                                                11-SEP-1985;
                                                                                                                                                                                                                                                                              W08601802-A
                                                                                                                                                                                                                                                                                                                          Malaria vaccine;
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                                   Disclosure; Fig 7; 55pp; English.
                                                                   poly:peptide(s) having
                                                                    DNA coding for Plasmodium falciparum antigens -
poly:peptide(s) having antigenicity of RESA or I
                                                                                                     N-PSDB;
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84AU-0007066
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                                                                                                                                                                                                                                                                                                                           antigen;
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 a novel DNA molecule which comprises corresp. to all or a portion of the
                                                                                                                                        Coppel
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                                                                         The present sequence is obtained from a clustral X alignment with CC protein 608. Protein 608 was identified using the method of the invention CC after subjecting rat osteoplasts to mechanical stress. Expression of the CC 608 gene was found to be upregulated by about 3-fold in cells subjected CC identification of genes responsive to a specific method for the CC identification of genes responsive to a specific mechanical stress. The CC method comprises applying the mechanical stress to an organism (tissue CC or cells comprising bone cells), isolating the specific cellular CC fractions and extracting mRNA from them, and differentially analysing the CC genes whose expression is responsive to a specific stress. The identification of genes whose expression is responsive to a specific stress. The identification genes whose expression is responsive to a specific stress. The identification genes are employed in determination methods are used for testing a controlling a physiological or disease state. The risk determination methods are used for testing or controlling a physiological or disease state (especially osteoporosis or CC controlling a physiological or disease state (especially osteoporosis or its symptoms or other conditions involved in mechanical stress or its bone development.
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                                                                  bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 32; Fig 6A-R; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identification of stress induced genes for determining risk and preventing, treating or controlling osteoporosis \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence g1/1017427/emb/CAA62189 from an alignment with protein 608
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Query Match Best Local Similarity Matches 266; Conserv

Conservative

9.2%; Score 627; DB 21; 24.1%; Pred. No. 6.9e-29; tive 110; Mismatches 442;

Length 4412; Indels 288;

Gaps

51;

Sequence

4412 AA;

MPRVRKPKTTPTP 918 	PEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTW apkeeaakpkgpikgvpkktpspieaerrklrpgsggekppdea	Qy 867 Db 4198	ם ס
TKKTITTTEIMNK 866 ; ; iaapvtvpvvgkkaeak 4197	TEKTTESKITAFTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTT	Qy 811 Db 4162	ם מ
PETTTAAPKMTKETATT 810 	LENSPKEPCYPTTKTPAATKPEMTTTAKDKTTERDLRTTP	4 .	
TTIHKSPDESTPELSAEPTPKA 754 : : : : svlrkrpeeeepkvepkk 4105	KKP-APTTPETPPPTTSEVSTPTTTKEP	405	
PTTPKEPAPTTP 705 : kifqlkaipkkkvpenp 4049	KEPAPTTPKKPARKELAPTTTKGPTSTTSDKPAPTTPKETA 	399	
PKEPAPTTPKGTAPTTL 652 : : : peepkkiipekkvp-vi 3992	KARKELARTITKEPTSTISDKPAPTTPKGTAPTTPKEPAPTT	399	
**XGTAPTTLKEPAPTTPK 592 ; ; 3vperaespppevye 3942		ω	
-TTPEEPAPTTPKAAAPNT 542 :: LVVPkkpeappakvpev 3889		w	
PKKLT 4		37	
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KKPAPTTPKEPAPTTPKE 371 	9 PTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKK 	Qу 31 Db 366	
<pre>IPKKPAPTTPKEPA 318 : </pre>	APTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT	- · · · · · · · · · · · · · · · · · · ·	
EP-APTTIKSAPTTPKEP 262 	LT :: iseki	. u 2	
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CAEVKDNKK 71 :: tavlelrdvakadsgdyv 3331	6 ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFC	Qy 2 Db 327	

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FX & X COOO OOO OOO OOO OOO OOO Claim vaccination and development of anti-mycobacterial . Fig 13; 55pp; English. agents

and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, monitoring vaccination, and for the development of vaccines and a high proline content, but there is no homology to any known a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see ANM31851-57) are claimed. These can be produced a proteins (see ANM31851-57) are claimed. These can be produced a proteins, especially in bacterial, yeast, fungal or This novel 74 kDa protein is encoded by an open reading frame a Mycobacterium tuberulosis DNA fragment (see AAT93610) contamolymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known monitoring vaccination, and anti-mycobacterial drugs. recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis containing The SP for

Sequence 763 AA;

Length 763;

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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire probes.
Sequence
                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                              Novel single exon nucleic in a human breast -
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Pred. No. 2e-38;
9; Mismatches 492;
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AC AAW4

XX AAW4

XX Mult

KW Cohe

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cc interact with the Cip subunit via conserved 23 amino acid dockerin co domains. Cip has been shown to contain 9 copies of a cohesin domain. CC The invention relates to the isolation of proteins binding to a novel coordinated a type II dockerin domain portion of Cip. The new CC I domain is designated a type II dockerin domain (as compared to the type CC I domain found on the catalytic subunits of the cellulosome). The type CC II dockerin domain has some sequence similarity to the type I dockerins compared to bind type I cohesin domains. CC The sequence presented here is an example of a protein which binds the novel type II dockerin and is the product of the OlpB gene. CC The protein contains 4 type II cohesin domains in the N-terminal portion CC of which the first domain (amino acid residues 28-192) is thought to bind CipA. The novel type II dockerin and cohesin domains can be used CC in complexes, especially enzyme complexes, to potentiate their catalytic actions in a synergistic manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                  cellobiohydratases, hemicellulases, e.g. xylanases or lichinases, whi interact with a central "scaffold" protein designated the cellulosome integrating protein (CipA; see AAW43108). The catalytic subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and conesins, which are two properties of such a complex is the cellulose degrading respectively. An example of such a complex is the cellulosome protein complex from Clostridium thermocellum, known as the cellulosome protein complex comprises around 15 proteins including endoglucanases, this complex comprises around 15 proteins including endoglucanases, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multimeric protein, especially enzymatic, complexes are held together by protein protein interactions between domains designated dockerins and cohesins, which are found on the catalytic and scaffold subunits respectively. An example of such a complex is the cellulose degrading
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 31-39; 60pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beguin P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lulase proteins with cohesin or dockerin type II domains - useful potentiating the activity of multiprotein enzyme complexes
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Sequence

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                                                                                               ----PTTTKEPAPT-TPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEP 474
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                                                                                                                                                                   TTPKEPA--PTTTKEPSPT-TPKEPAPTTTKS-APTTTKEPAPT---TTKSAPTTPKEPS 419
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Pred. No. 1.1e-48;
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Matches 364
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06-APR-1999

06-APR-1999

16-APR-1999

19-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

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27-MAY-1999;
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hybridisation assay; genetic mapping; gene expression control;
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19-MAY-1999;
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promoter;
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                                                                                                                                                                                                                                                                                                                           This sequence represents the human megakaryocytopoientin (MPO) protein. This sequence was purified using a carrier which can couple wheat germ agglutinin and heparin to separate MPO. Fragments of this sequence (see AR80039 and AAR80040) were used to produce the amplification primers can then be used as probes to screen human cDNA libraries for MPO cDNA. The MPO cDNA can then be inserted into a plasmid which is used to canny formation of megakaryocytes, enlarging the size of promoting colony formation of megakaryocytes, enlarging the size of megakaryocytes and stimulating the proliferation of multipotential stem cells. The purification method can be used to isolate MPO from human urine or come of patients with aplastic anaemia, and from animal blood or urine the pradiation stimulation and the matocytopenia.
                                                                                                                                                                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New haematopoietic cell growth factor - used for treating thrombocytopenia and hematocytopenia {\sf T}
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328; Conserv
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Pred. No. 1.9e-91;
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The present invention describes colon tumour associated proteins (I) and (II) and (II) can be used in gene therapy and vaccine production. (I) and CI may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) color used to treat disorders associated with decreased expression by coloric cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by coloric cancer. For example, (I) and (II) may be rectifying mutations or deletions in a patient's genome that affect the cativity of TCAPs by expressing inactive proteins or to supplement the produce the TCAP production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used to down regulate. TCAP expression and activity. The anti-(I) antibodies may also be used to down regulate as diagnostic agents for detecting the presence of TCAPs in samples.
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19-MAY-2000;
29-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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15-FEB-2000;
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                                                                                                                                                                                                                                                                                                                             TNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFK 1129
                                                                                                                                                                                                                                                                                                                                                                   {\tt gtlvafrghyfwmlspfsppsparritevwgipspidtvftrcncegktfffkdsqywrf}
                                                                                                                                                                                                                                                                                                                                                                              GTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRF
          2001-182721/18
                                                 UNIV
                                                                                                                                                                                                                                                                             standard; Protein; 472
                                                  CASE
                                                                                                                                                                                                                                         (first entry)
                                                                      2000US-0145328
                                                                                99US-0145328
                                                   WESTERN RESERVE
                                                                                                                                                                                                                     superficial zone protein
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New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, us treating osteoarthritis, or as lubricants of tissue and joints
                                                                 useful
                                                                 tor
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Example 1; Fig 4; 34pp; English.

The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathy-according to a vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous being megakaryocyte stimulating factor (MSF). The gene encoding cacp protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-this gene are responsible for the heritable disorder camptodactyly-arthropathy-coxa vara-pericarditis, in which patients have synovial arthropathy-coxa vara-pericarditis, in which patients have synovial acts as a synovium lubricant, and can be used to lubricate tissue and joints in the treatment of osteoarthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence represents the bovine orthologue of human MSF, superficial zone protein (SZP).

Sequence 472 A,

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                                                                                       alslaqyksrpesvyffkrggsvqqytykqeptqkctgrrpainysvygetaqvrrrfe
                                                                                                     ALSTAKYKNWPESVYFFKRGGS1QQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFE 1171
                                                                                                                                 DYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1270
                                                      RAIGPSOTHTIRIQYSDARLAYODKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGY
dyyalskdqyynidvpsrtaraittrsgqtlsntwyncp
                                          {\tt raigpsqvhtirihytpvrvpyqdkgflhnevkvstlwrglpnvvtsaislpnirkpdgy}
                                                                                                                                                                                                                                                                                                                      Similarity 79.9
                                                                                                                                                                                                                                                                                                                               25.1%; Score 1707.5; DB 22; Length 472; 79.9%; Pred. No. 1.2e-94;
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10-APR-1996

entry)

megakaryocytopoientin

protein

Human; megakaryocytopoientin; wheat germ agglutinin; heparin; megakaryocyte; aplastic anaemia; thrombocytopenia; hematocytopenia; multipotential stem cell.

AAR80041

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AAR80041 standard;

Protein;

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RESULT

AAB29778

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                                                     Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic.
          24-APR-2000;
                     02-NOV-2000
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                                                                                      Human MSF-derived tribonectin
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          2000WO-US10953
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Query Match Best Local Sim Matches 794;

Similarity

Length

Conservative

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The invention relates to a human tribonectin which is a product of CC gene. The tribonectin has at least one o-linked oilgosaccharide CC gene. The tribonectin has at least one o-linked oilgosaccharide CC lubricating molety and has a polypeptide sequence comprising 1-76 CC (AAB29774). The invention also relates to a nucleic acid encoding a CC (AAB29774). The invention also relates to a nucleic acid encoding a CC human MSF-derived tribonectin; a blocompatible composition comprising a CC of diagnosing osteoarthrikis or a predisposition to osteoarthritis by CC measuring the amount of MSF or its fragment in a biological sample of a confidence the presence of or predisposition to developing control control content fritis. The tribonectin and DNA encoding it are useful in the CC mammalian joints, such as articulating joints of humans, dogs or horses. CC tribonectin, when formulated as a membrane, foam, gel or fibre, is cuseful for inhibiting adhesion between two surfaces such as the injured cor trauman, or an artificial device e.g., an orthopaedic implant. In CC particular, one of the surfaces is pericardial tissue. DNA encoding a cc a substantial portion of a human MSF-derived tribonectin.
  Sequence
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       TEKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPAPTTPEEPAPTTPKAAAPNTPKE
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                               paptt-kepaptt-kepaptt-kepap-ttkepaptt-kepaptt-kepapt
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                                                                                                                                                                                              51.1%; Score 3484; I
74.6%; Pred. No. 1.30
tive 28; Mismatches
DB 22;
1.3e-200;
les 80;
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                                                               Homo
                                                                             biodiversity;
                                                                              Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                Human EST encoded protein SEQ
                                                                                                                                12-OCT-2001
                                                                                                                                             AAM24322;
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25-JAN-2000;
17-JUL-2000;
                    25-JAN-2001; 2001WO-US02687
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2000US-0491404
2000US-0617746
                                                                                                                                (first entry)
                                                                                                                                                            Protein;
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                                                                                                                   NO: 1847.
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N-PSDB;
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15-SEP-2000;
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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a
                                                                                                                                                                                                                                Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety
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CC human MSF-derived tribonectin; a biocompatible composition comprising a CC human tribonectin for inhibiting tissue adhesion formation; and a method CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by CC measuring the amount of MSF or its fragment in a biological sample of a CC indicates the presence of or predisposition to developing CC osteoarthritis. The tribonectin and DNA encoding it are useful in the CC treatment of osteoarthritis, where they may be used for lubricating CC mammalian joints, such as articulating joints of humans, dogs or horses. CC useful for inhibiting adhesion between two surfaces such as the injured CC tissues of a mammal, where the injury is caused by a surgical insertion CC or trauma, or an artificial device e.g., an orthopædic implant. In CC particular, one of the surfaces is pericardial tissue. DNA encoding a CC tribonectin may be used in gene therapy. The present sequence represents
  Sequence
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                                      The invention relates to a method of treating osteoarthritis via the CC administration of a composition comprising the camptodactyly-arthropathy. CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous conjection. The human CACP protein is identified in the invention as the protein (MSF) is located on chromosome 1925-31, and mutations in this gene are responsible for the heritable disorder camptodactyly constraints without evidence of inflammation. CACP protein (MSF) carthropathy-coxa vara-pericarditis, in which patients have synovial conditions in the treatment of osteoarthritis. The composition may be consisted to reduce the symptoms of osteoarthritis (e.g., joint pain, consisted to reduce the symptoms of osteoarthritis (e.g., joint pain, consisted to lower the pain, consisted the symptoms of osteoarthritis (e.g., joint pain, consisted to lower the pain, consisted the pain, 
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The sequence given is a full length translation from the megakaryocyte of stimulating factor (MSF) precursor. The sequence covered by exons II, and IV encodes megakaryocyte stimulating factor (MSF). This considered by the addition of an N-terminal sequence encoding the ministry leader, an initiating methionine proceeding exon II and a secretory leader, an initiating methionine proceeding exon II and a sequences derived from human megakaryocyte colony stimulating factor (Meg-CSF). Exon I contains the initiating methionine, and encodes a concoding the original meg-CSF includes exons II-IV and is thought to terminate in the region between amino acid residues 134 - 147. The contains the initiating methionine, and encodes a concoding the original meg-CSF includes exons II-IV and is thought to primary transcript of this gene may be cleaved in different ways to valid a family of mRNA's each encoding a different ways from the processing of the sequence of the calso implicated in the stability, folding and processing of the consecute of the resulting factor, is one or more of these exons may contain the processing or folding of the appropriate structure of the resulting factor, is one or more of these exons may contain the consecution of the cellular matrix or extracellular matrix processing. Both naturally cocuring MSF's may be characterised by carlous combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different combinations.
                                                                                                                                                                                                               Query Match 98.7
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Matches 1270; Conservative
121 ppsgasqtiksttkrspkppnkkktkkvleseelteehsvsenqessssssssssssstiw 180
                                                                                                                                                                                                                                                                                                           Sequence
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Page 16

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The present sequence is encoded by an intestinal insect mucin (IIM) co isoform IIM22. The isoforms IIM22 and IIM14 (see AAZ45836) are nearly co identical isoforms. The proteins are identical except for slightly co different peptide lengths in some repetitive regions, which is common communication proteins. The IIM cDNA sequence was identified and cloned from common common in larval peritrophic membrane (PM). The IIM polypeptides are useful in the production of transgenic or combinant vectors which express e.g. the polypeptide or antibodies confired against it. Such vectors are useful to produce IIM proteins, commission proteins and portions of IIM to disrupt the PM.

CC vectors comprising DNA encoding anti-IIM antibodies can especially be used to protect plants against insect pests having an IIM protein in common comparison of their midgut. The vector could be used to enhance the defenses of comparison plants or enhance the effectiveness of bio-engineered comparison of the vector could be used to enhance the defenses of comparison plants or enhance the effectiveness of bio-engineered comparison of the produced. Since IIM was shown to be degraded in vivo in T. ni larvae by enhancin (which is encoded and comparison period by specific baculoviruses and known to facilitate entry of virus centarion-like entry of virus enhancin-like entry ent
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490 apta----aptaaptaaptaaptaapstvvppatppataapvppttaiptpaptaaptaa
                                                                                            430 llphesdcggylqcvhgqtiarpcpgnlhfspatqscespvtagcqvfecdsdnqctsta 489
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nes 215; Conserv
                                                                                                                                                                                          elqqcdhielvgctlpggeseevdvdedactgwycptepieweplp---ngcpadfsidh 429
                                                                                                                                                                                                                                                                                                                                                                                       dfdihlliphdkycnlfyqcsngytfeqrcpeglyfnpyvqrcdspanvecdgeispapp 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tttq--aptttqaptttt---qapttttq-apttttqaptttq--aptttq--aptttqa 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIPKEPAPTITKEPAPTTPKEPAPTITKEPAPTTTKSAPITPKEPAPTTPKKPAPTTPKE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vtegnededidigdlldngcpanfeidwllphgnrcdkyyqcvhgnlverrcgagthfsf 372
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                              APTIPKEPAPTTPKKPAPTIPKEPAPTTPKEPA-PTTIKKPAP--TAPKEPAPTIPKETA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               807 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 542; DB 21; Length 807; 30.4%; Pred. No. 4.8e-23; tive 23; Mismatches 194; Indels 276;
                                                                                                                                                    -TTKEPAPTTTKSAPTTPKEPSPTT----
                                                                                                                                                                                                                                                  ----PTTP--KEPAPTTTKSAPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PTTPKEPAPTTPK----EPAPT 310
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                  KKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKP 643
                                                                                                                                                                                                            pttaapesptt-----vtvpptaapta----apttavpeipitvt---saptaaptaapt
                                                                                                     TTTKEPTST-TSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTP 595
ah----apnttaapvttts---apattpedddidp--plpndpinp 720
                                                                  tvtvpptaapttaapap----nttvtapptaaptt-aapapnttvtvpptaaptaapptv 683
                                                                                                                                                            TPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAP 536
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11-SEP-1984;
10-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                         The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA and FIRA have antigenicity suitable for providing protective immunity against Plasmodium falciparum malarial infections.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 7; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding for Plasmodium poly:peptide(s) having ant falciparum
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N-PSDB; AAN60473.
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KEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLT
                    tqepvtveehidekkgsegdnislsslseeteekshtkkkksswlkfgrgnkndkkskne
                                                 TKEPAPT -
                                                               pvtt----qepvtiee--pvttqepvtieepvttqepvttqepvttqep---vttqepvt
                                                                              PAPTAPKKPAPTTPKEPAPTTPKEPA----SPTTPKEPAPTTTKSAPTT
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                                                                                                                                 TTPKEPA----PTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPA----PTTPKE
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                                             -TTKSAPTTPKEPSPTTTKEPA----
                                                                                                                                                                                                                                                                                                                                          Score 544; DB 7;
Pred. No. 3.9e-23;
10; Mismatches 342
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of RESA or 1
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    expressing
FIRA antigens

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 24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                    Intestinal insect mucin; IIM; isoform; IIM14; peritrophic membrane;
insect pest; transgenic plant; IIM22; bio-engineered pesticide;
enhancin; insect vector.
                             23-JUN-1999;
                                                         29-DEC-1999
                                                                                                                                  Misc-difference
                                                                                                                                                              Misc-difference
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                             99WO-US14220
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43
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                                                                                                                                                                                                                       /note= "unspecified amino acid 42
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                     New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                  AAW31855;
Claim 11; Fig 16;
                                                                                                              Espitia C,
                                                                                                                                       (GBFB )
                                                                                                                                                                29-APR-1996;
                                                                                                                                                                                         18-APR-1997;
                                                                                                                                                                                                                06-NOV-1997
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                                                                                                                                                                                                                                                                  Mycobacterium
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                                                                                                                                                                                                                                                                                                      Tuberculosis; mycobacteria; infection; diagnosis;
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DB; AAT93610.
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                                                                                                                                        GBF GES BIOTECH FORSCHUNG GMBH.
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55pp; English
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RESULT 1
AAP60570
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AAP60570

standard;

Protein;

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24-AUG-1991 AAP60570;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Mechanical stress; gene therapy; protein 608; osteoporosis; bone density; bone development; g1/1017427/emb/CAA62189.
                                                Sequence g1/1017427/emb/CAA62189
                                                                                22-FEB-2000
                                                                                                                AAY53666
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The present sequence is obtained from a clustral X alignment with protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular fractions and extracting mRNA from them, and differentially analysing the mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a modificancy for the state of th
                                          medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis obone density or other factors causing or contributing to osteoporosis its symptoms or other conditions involved in mechanical stress or its lack. The methods can also be used for advancing research or studies in
bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 32; Fig 6A-R; 308pp; English.
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                                                                                                       a MyCODACCELLAM. CO. 1 A MYCODACCELLAM. CO. 1 A MYCODACCELLAM. CO. 1 A high proline content, but there is no homology to any known a high proline content, but there is no homology to any known a high proline-rich antigens of mycobacteria. Novel M. tuberculosis proline-rich antigens of mycobacteria. These can be produced as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1129
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                                      recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and monitoring vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1188 tlttetikapvkstenpekt 1207
                                                                                                                                                          This novel 74 kDa protein is encoded by an open reading frame a Mycobacterium tuberulosis DNA fragment (see AAT93610) contai polymorphic GC-rich sequences. Its amino acid sequence shows
                                                                                                                                                                                                                                              New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antimycobacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW31852 standard; Protein;
                                                                                                                                                                                                                                                                                                        WPI; 1997-549750/50
N-PSDB; AAT93610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculosis; mycobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
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Sequence
                           anti-mycobacterial
                                                                                                                                                                                                                    Claim 5; Fig 13; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                             (GBFB ) GBF GES BIOTECH FORSCHUNG
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                              drugs.
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Query Match Best Local Similarity Matches 248;

14.3%; 28.2%;

Score 715; DB 18; Pred. No. 8.9e-33; 99; Mismatches 361;

Length 763; Indels

232;

Gaps

39;

Conservative

39;

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CC and cohesins, which are found on the catalytic and scaffold subunits CC respectively. An example of such a complex is the cellulose degrading CC protein complex from Clostridium thermocellum, known as the cellulosome. CC rhis complex comprises around 15 proteins including endoglucanases, cc cellobiohydratases, hemicellulases, e.g. xylanases or lichinases, which integrating protein (CipA; see AAW43108). The catalytic subunits complex comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellulase proteins with cohesin or dockerin type II domains - useful for potentiating the activity of multiprotein enzyme complexes
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interactions between domains designated
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Pred. No. 3.5e-45;
B3; Mismatches 312
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                                The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, staying, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not specification, but was obtained in electronic fo
                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                    Penn
                                                                                                                                                                                                               Novel single exon nucleic acid in a human breast -
                                                                                                                                                                                      Claim 27;
                                                                                                                                                                                                                                                                                                                                        27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
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                                                                                                                                                                                                                                                                                                            (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #2327 encoded by probe for measuring breast gene expression
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                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS INC
                                                                                                                                                                                SEQ ID No 12385; 322pp;
                                                                                                                                                                                                                                                                                 Hanzel
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2000US-0608408
2000US-06323686
2000US-0234687
2000US-0234687
2000US-0236359
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast disease; breast cancer;
                                                                                                                                                                                                                                                                                 DK,
                                                                                                                                                                                                                                                                               Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                               ξ
                                                                                                                                                                                                                   probe used to measuring gene expression
                                                                                                                                                                                                                                                                               Rank DR;
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20-SEP-1999

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   255
                            lpptippetpptgppatpptevlptgpptlppqtpptippeippntppqtpptlp----p
 TTPKEPTPTTPKEPAPTT-KEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTK 313
                                             PAPTTTKEPAPTTPKEPAPTTTKEPAPTT--TKSAPTTPKEPAPTTPKKPAPTTPKEPAP
                                                                                  qtqaqnrpylrpppprippppcpvctcp-epsp------pppptvt---pqippt 170
                                                                                                                   ETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKE 196
                                                                                                                                                    226;
                                                                                                                                                  Similarity 38.5
26; Conservative
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99US-0158369.
99US-0159293.
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99US-0150566
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99US-0161989
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99US-0159584.
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                                                                                                                                                                  19.6%;
                                                                                                                                                    24;
                                                                                                                                                    Score 981; DB 21;
Pred. No. 1.1e-47;
4; Mismatches 293;
                                                                                                                                                                                Length 763;
                                                                                                                                                       Indels
                                                                                                                                                       44;
                                                                                                                                                       Gaps
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                                       226
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multimer; enzyme; complex; protein-protein interaction; dockerin domain; cohesin domain; catalytic subunit; scaffold subunit; SdbA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. thermocellum OlpB protein.
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                         WPI; 1998-011569/02.
N-PSDB; AAT86623.
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                                                                                            Beguin P,
                                                                                                                                                                                                                                      10-MAY-1996;
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Best Local
                                                                                                                                                                                     produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples
                                                                                                                                                                                                                                                                                                                                                                    expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                               (I) and (II) can be used in gene therapy and vaccine production. (I) an (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 446-462; 472pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu J,
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immunogenic; gene therapy; vaccine; colonic cancer.
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                                                                                                                                          g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512
AAM24494 to AAM24523 represent nucleotide and amino acid sequences
en in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes colon tumour associated proteins (I) and polynucleotides (II) that encode them. (I) have cytostatic activity.
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Best Local Similarity 88.3
Matches 263; Conservative
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                                                                                                           TLAPKYTTTKKTITTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKT
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                                                mprvrkpkttptprkmtstmpelnptsriaeamlqtttrpnqtpnsklvevnpksedagg
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Pred. No. 1.6e-273;
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Вþ 20

61 _ QV

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PRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK 120

Matches Query Match Best Local

Local Similarity hes 672; Conser

Conservative

28;

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Indels

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arcernative splicing; joint osteoarthritis; tribosummler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating figure. The tribonectin has at least one O-linked oligosaccharide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1999;
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28; Mismatches
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                                                  22;
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Injection. The human CACP protein is identified in the invention as the being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1925-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-carthropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) carts as a synovium lubricant, and can be used to lubricate tissue and Joints in the treatment of osteoarthritis. The composition may be capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis (e.g., joint pain, capplied to reduce the symptoms of osteoarthritis.
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CC The invention relates to a human tribonectin which is a product of CC alternative splicing of the human MSF (megakaryocyte stimulating factor) Gene. The tribonectin has at least one O-linked oligosaccharide CC lubricating molety and has a polypeptide sequence comprising 1-76 CC repeats of a motif having at least 50% identity to the sequence KEPAPTT CC (AAB29774). The invention also relates to a nucleic acid encoding a CC human MSF-derived tribonectin; a biocompatible composition comprising a CC human MSF-derived tribonectin; a biocompatible composition comprising a CC human further control of MSF or its fragment in a biological sample of a CC diagnosing osteoarthritis or a predisposition to osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a CC indicates the presence of or predisposition to developing osteoarthritis. The tribonectin and DNA encoding it are useful in the CC mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured CC issues of a mammal, where the injury is caused by a surgical insertion cor tribonectin may be used in gene therapy. The present sequence represents
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lubricant; O-linked oligosaccharide;
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cc (meg-CSF). Exon I contains the initiating methionine, and encodes a CC classical mammalian protein secretion signal sequence. The sequence cc encoding the original meg-CSF includes exons II-IV and is thought to cterminate in the region between amino acid residues 134 - 147. The CC primary transcript of this gene may be cleaved in different ways to CC yield a family of mRNA's each encoding a different MSF protein. Exons CC V and VI are thought to be related to the activity of the factor and CC are also implicated in the stability, folding and processing of the CC synergy of MSF with other cytokines. Exons V - XII are believed to be implicated in the processing or folding of the appropriate structure of the resulting factor, ie. one or more of these exons may contain CC sequences which direct proteolytic cleavage, adhesion, organisation of the cellular matrix or extracellular matrix processing. Both naturally occuring and non-naturally occuring MSF's may be characterised by with the exons spliced together in differing orders to form different commembers of the MSF family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is modified by the addition of an N-terminal sequence encoding a secretory leader, an initiating methionine proceeding exon II and a terminating codon following exon IV. The cDNA sequence given contains sequences derived from human megakaryocyte colony stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence given is a full length translation fr
stimulating factor (MSF) precursor. The sequence
III and IV encodes megakaryocyte stimulating factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK
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                                                                                                                                                                                                                                                                                                                 PTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKSAPTTTKSAPTTPKEPSPTTTKE
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PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK 540
                                                                                             TPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKE
                                                                                                                                                                                                                                                                                                                                                               pkkpapttpkepapttpkeptpttpkepapttkepapttpkepaptapkkpapttpkepa
                                                                      tpkkltpttpeklapttpekpapttpeelapttpeeptpttpeepapttpkaaapntpke
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The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous

Example 1; Page -; 34pp; English.

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                                                                                                                                                                                        New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2001
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19-JUL-2000;
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stimulating factor; synovial lubricant;
; osteoarthritis; joint lubrication; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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Query Match
Best Local S
Matches 941
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 TERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTT
                                                                                                                                                                                                                                                \verb|ptttkepttihkspdestpelsaeptpkalenspkepgvpttktpaatkpemtttakdkt|
                                           PTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKT
                                                                                    KELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVST
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                                                                                                                              EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKXPAP
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nilarity 100.0%;
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New human mega-karyocyte
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10-SEP-1991;
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DB; AAQ27223.
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proteolytic cleavage; adhesion; alternative splicing.
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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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Gapop 10.0 ,
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 4 4 6 6 7 7 10	Result
5011 5011 5011 5011 2012.5 1357.5 1357.5 1357.5 1942 771.5	Score
100.0 100.0 100.0 100.0 276.1 27.1 23.3 19.6 18.8 15.4	Query Match Length DB
1299 1404 1404 1400 902 452 5179 763 1664 1325 763	ength [
13 12 22 22 16 22 19 19 18	1
AAM24322 AAR26049 AAB60568 AAB29778 AAB29778 AAR80041 AAM24516 AAG38942 AAW43106 AAM03645 AAM03645	ID
Human EST encoded MSF precursor. Sy Human megakaryocyt Human megakaryocyt Human megakaryocyt Human MSF-derived Human megakaryocyt C899p predicted am Arabidopsis thalia C. thermocellum Ol peptide #2327 enco Mycobacterium tube	Description

287
963
AAI 1/400 AAB22934
G83007
AAR80839
Y95556
Y95559
B60569
Y05477
AAR14162
AAR14160
B11727
AAW48299
M02607
AAM27312
AAM14883
AAP82974
AAB95541
AAM24513
AAY59288
AAM04187
V116458
326042
350362
AAB50363
AAB11726
341231
AAP82975
AAY54466
AAY54467
С
AAW31855
Y53666

ALIGNMENTS

RESULT

710011)
AAM24322	
Đ	AAMZ43ZZ Standard; Frocein; 1233 AA.
XX	
AC	AAM24322;
XX	
DΤ	12-OCT-2001 (first entry)
XX	
DE	Human EST encoded protein SEQ ID NO: 184/.
××	Table 1
ΚW	Human; sheep; pig; cow; fruit tly; yeast; namster; macaque; nurse;
ΚW	tomato; monkey; dog; sea urchin; expressed sequence ray; Esti
ΧZ	diagnostics; forensic test; gene mapping; genetic disorder;
ΚW	biodiversity; gene therapy; nutrition.
XX	
SO	Homo sapiens.
XX	WOODON 577-29
4 2	
3 >	03-316-2001
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ΡF	25-JAN-2001; 2001WO-US02687.
XX	
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PΑ	(HYSE-) HYSEQ INC.
ΡX	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
ΡI	ĸ
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DR	WPI; 2001-476164/51.

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Search completed: April 26, 2002, 16:16:16 Job time: 167 sec

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RESULT 1
AAB60569
ID AAB60569
XX AAB6
XX AAB6
XX AAB6
XX BOV1
XX BOV1
XX BOV1
XX BOV1
XX BOV2
XX WO2(

                                                                       COXA vara-pericarditis (CACP) protein, or portions of the CACP protein.
CC The composition may further comprise a local anaesthetic The composition of the invention may be administered via intra-articular or intravenous in the invention may be administered via intra-articular or intravenous composition.
CC injection. The human CACP protein is identified in the invention as composition of the invention as in this protein (MSF). The gene encoding composition composition in the invention as composition of the symptoms in this gene are responsible for the heritable disorder camptodactyly-cc arthropathy-coxa vara-pericarditis, in which patients have synovial composition as a synovium lubricant, and can be used to lubricate tissue and composition the treatment of osteoarthritis. The composition may be composed to reduce the symptoms of osteoarthritis (e.g., joint pain, composition than the present sequence composition than the bovine orthologue of human MSF, superficial zone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly arthropathy-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1;
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19-JUL-2000; 2000US-0145328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCA-) UNIV CASE WESTERN RESERVE.
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                                                                (SZP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 4; 34pp; English.
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Query Match Best Local Similarity

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11-SEP-1984;
10-SEP-1985;
                                                                                                                                             The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (AAM60472) or FIRA (AAM60473). RESA and F. antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.
                                                                                                                                                                                                                                                                                                Kemp
                                                                                                                                                                                                                             DNA coding for Plasmodium falciparum antigens - poly:peptide(s) having antigenicity of RESA or Ffalciparum
                                                                                                                               Sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proline rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAM31851-57) are claimed recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a Mycobacteria. The amino actually polymorphic GC-rich sequences. Its amino actually to any known a high proline content, but there is no homology to any known a high proline content, but there is no homology to any known a high proline content, but there is no homology to any known a high produce.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
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                                                                                                                                                                                                                                                   TKSAPTTPK-EPSPTTTKEP--APTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTK
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ppapn--rppappap--pappel---
                                   GTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTP
                                                                    mpalp--pappsppatrlcpplppsppapnsp--pappap----ptppkllsanppcppv
                                                                                           TPTTPEEPAPTTPKA---AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPK---ETAPTTPK
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SKATTPKPQKP----TKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTM-----PELNP
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                                                                                                                                                                                                                                                                                                                                                                                                             KEPAPTTP----KKPAPKELAPTTTKGP-TSTTSDKPAPTTPKET---APTTPKEPAPTTP
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99 TDGKEKTTSAKETQSIEKT-----SAKDLAPTSKVLAKPTPKAETTTKGPALT-----

Query Match

Local Similarity 26.2 nes 225; Conservative

12.1%;

Score 625.5; DB 21; Pred. No. 4.8e-27; Mismatches 379;

Indels 169; Length

Gaps

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Sequence

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The present sequence is obtained from a clustral x alignment with CC protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the CC 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the CC identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue CC cor cells comprising bone cells), isolating the specific cellular CC mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identify CC genes whose expression is responsive to a specific stress. The identify CC genes are employed in determining risk associated with a physiological or CC disease state. The risk determination methods are used for testing a cc method of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or bone density or other factors causing or contributing to osteoporosis or controlling a physiological or causing or contributing to osteoporosis or bone density or other factors causing or contributing to osteoporosis or
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                                                  bone density or other factors causing or contributing to osteoporosits symptoms or other conditions involved in mechanical stress or it lack. The methods can also be used for advancing research or studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identification of stress induced genes for determining preventing, treating or controlling osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 32; Fig 6A-R; 308pp; English.
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gi/1017427/emb/CAA62189.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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Pred. No. 9.1e-36;
7; Mismatches 466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
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                                                                                                                                                    New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring
                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                      Espitia
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Domain

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interact with a central "scaffold" protein designated the cellulosome

integrating protein (CipA; see AAW43108). The catalytic subunits

integrating protein (CipA; see AAW43108). The catalytic subunits of a cohesin domain.

Integrating protein conserved 23 amino acid dockerin

conserved 23 amino acid social domain.

The invention relates to the isolation of proteins binding to a novel

conserin type domain found in the C-terminal portion of Cip. The new

condain is designated a type II dockerin domain (as compared to the type

If domain found on the catalytic subunits of the cellulosome). The type

If dockerin domain has some sequence similarity to the type I dockerins

but is unable to bind type I cohesin domains.

The sequence presented here is an example of a protein which binds

the novel type II dockerin domain sin the N-terminal portion

of which the first domain (amino acid residues 28-192) is thought to

bind CipA. The novel type II dockerin and cohesin domains can be used

in complexes. essentially enzyme commission to the color of the color o
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Best Local S
Matches 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellulase proteins with cohesin or dockerin type II domains for potentiating the activity of multiprotein enzyme complex
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mes 276; Conserv
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   sdeptpsdeptpsdeptpsetpeepiptdtpsdeptpsdeptps----
                                     TTPKEPA--PTTTKEPSPT-TPKEPAPTTTKS-APTTTKEPAPTTTKSAPTTPKEPSPTT : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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Pred. No. 3e-45;
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27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                     MOLECULAR DYNAMICS INC
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                                             ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
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09-AUG-1999; 10-AUG-1999; 11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999;

16-AUG-1999; 17-AUG-1999; 02-AUG-1999 03-AUG-1999 04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 09-AUG-1999

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S-0147260. S-0147303. S-0147416.

99US-0147204. 99US-0147302. 99US-0147192. 28-JUL-1999; 02-AUG-1999; 02-AUG-1999;

99US-0145951. 99US-0146386. 99US-0146388.

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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                       Multimer; enzyme; complex; protein-protein interaction; dockerin domain; cohesin domain; catalytic subunit; scaffold subunit; SdbA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.
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99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                           /note= "cohesin type 207..363
                                                                                Location/Qualifiers 28..192
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Pred. No. 8.9e-48;
4; Mismatches 293
        type II domain"
                                                          II
                                                            domain"
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10-SEP-1999; 13-SEP-1999; 15-SEP-1999; 16-SEP-1999;

99US-0147433.
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99US-0148171.
99US-0148565.
99US-014926.
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99US-0160980.
99US-0161406.
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20-SEP-1999
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18-AUG-1999;
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31-AUG-1999;

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9908-0123180

9908-0125788

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19-MAY-2000;
29-JUN-2000;
                      (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the rectifying mutations or deletions in a patient's genome that affect the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM24516 standard;
                                                                                                                                                                                                                                                                                                                                                                                     Claim
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15-FEB-2000;
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polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AA128460 to AA12951 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
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                 This sequence represents the human megakaryocytopoientin (MPO) protein. This sequence was purified using a carrier which can couple wheat germ aggluthnin and heparin to separate MPO. Fragments of this sequence (see AAR80039 and AAR80040) were used to produce the amplification primers shown in AAF04544 and AAF04545. The fragments amplified by these primers can then be used as probes to screen human cDNA libraries for MPO cDNA. The MPO cDNA can then be inserted into a plasmid which is used to transform cells to produce MPO. The MPO sequence is capable of promoting colony formation of megakaryocytes, enlarging the size of megakaryocytes and stimulating the proliferation of multipotential stem cells. The factor may be used for treating thrombocytopenia and hematocytopenia. The purification method can be used to isolate MPO from human urine or serums of patients with aplastic anaemia, and from animal blood or urine by radiation exposing the animals to induce aplastic anaemia.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one o-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of diagnostic content for inhibiting tissue adhesion formation; and a method of diagnostic content for inhibiting tissue adhesion formation; and a method of diagnostic content of the sequence of 
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osteoarthritis. The tribonectin and DNA encoding it are useful in the treatment of osteoarthritis, where they may be used for lubricating mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant. In
                                                                                                                                                                                                                                                                                 of diagnosing osteoarthritis or a predisposition to osteoarthritis measuring the amount of MSF or its fragment in a biological sample mammal, wherein an increased amount of MSF compared to a control indicates the presence of or predisposition to developing
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coxa vara-pericarditis (CACP) protein or portions of the CACP protein.

CC The composition may further comprise a local anaesthetic. The composition
cC of the invention may be administered via intra-articular or intravenous
clipetion. The human CACP protein is identified in the invention as
cC being megakaryocyte stimulating factor (MSF). The gene encoding
cC CACP protein (MSF) is located on chromosome 1925-31, and mutations in
cC this gene are responsible for the heritable disorder camptodactyly-
cC arthropathy-coxa vara-pericarditis, in which patients have synovial
cC hyperplasia without evidence of inflammation. CACP protein (MSF)
cC acts as a synovium lubricant, and can be used to lubricate tissue and
cC joints in the treatment of osteoarthritis. The composition may be
cC applied to reduce the symptoms of osteoarthritis (e.g., joint pain,
cC loss of range of movement or joint damage). The present sequence
cC represents human megakaryocyte stimulating factor (MSF, CACP protein).
cC specification, although a GenBank accession number was given. This
cc sequence was therefore obtained from GenBank (U70316).
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             The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MSF; megakaryocyte stimulating factor; tribonectin; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC III and IV encodes megakaryocyte stimulating factor (MSF). This covered by the addition of an N-terminal sequence encoding CC sequence is modified by the addition of an N-terminal sequence encoding CC terminating codon following exon IV. The cDNA sequence given contains CC (meg-CSF). Exon I contains the initiating methionine, and encodes a CC classical mammalian protein secretion signal sequence. The sequence cc encoding the original meg-CSF includes exons II-IV and is thought to CC terminate in the region between mainto acid residues 134 - 147. The CC yield a family of mRNA's each encoding a different ways to CC vield a family of mRNA's each encoding a different MSF protein. Exons CC vield a family of mRNA's each encoding a different MSF protein. Exons CC vield a family of the stability, folding and processing of the complicated in the stability, folding and processing of the CC synergy of MSF with other cytokines. Exons V - XII are believed to be cimplicated in the processing or folding of the appropriate structure of the resulting factor, ie. one or more of these exons may contain CC sequences which direct proteolytic cleavage, adhesion, organisation of the cellular matrix processing. Both naturally occurring and non-naturally occurring mSF's may be characterised by carfous combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different CC members of the MSF family.
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68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 5155; DB 13; 100.0%; Pred. No. 4.2e-282; tive 0; Mismatches 0;
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New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint:

joints

useful

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Query Match
Best Local Sim
Matches 968;
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10-SEP-1991;
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  Gesner
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proteolytic cleavage;
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                                            91US-0643502
91US-0757022
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67..107
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1373..14
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1331..1:
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157..200
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TG,
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.1212
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Hewick
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adhesion; alternative splicing.
Jacobs
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 VKDNKKNRTKKKPTPKPPVV......GKPVDGLTTLRNGTLVAFRG
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                                                                                                                                                                                                                                                                                                                                                                  : /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT: *
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Copyright (c) 1993 - 2000 Compugen Ltd
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 AAM24322
AAR26049
AAB6968
AAB29778
AAB29778
AAAB29778
AAAB298216
AAG38942
AAW43106
AAM31852
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                                                                                                                                                                                                                                                                      SUMMARIES
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                                      Human megakaryocyt
C899P predicted am
Arabidopsis thalia
C. thermocellum Ol
                                                                                                                                                                                                                Description
                                                                                                           Human
Human
                                                                                                                                        Human EST encoded
MSF precursor. Sy
Human megakaryocyt
                    Peptide #2327
                                                                                                           megakaryocyt
MSF-derived
     enco
tube
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EXFU-DEVD-MAP4-EBE	AAB22870	21	61			
icrotubule asso	79	21	1125	8.2	424.5	
Mouse microtubule-	293	21	12			
n atrophin-i	740	20	01			
idermidis op	8300	22	ы			
apanese sea m	80	16	Uī			
-	555	21	7			
s O	AAY95559	21	2870			
. albicans Kbti	547	20	750		46	
RP encoded by CI	41	12	378		46	
378. Triti	16	12	378		50	
Peptide #1289 enco	0	22	511		467.5	
Peptide #1349 enco	AAM27312	22	511	9.1	67	
Peptide #131/ enco	188	22	511	•	67.	
ve pre	AAP82974	9	652		9	
Human p	AAB95541	22	1127		\sim	
S	AAW48299	19	1721		~	
predicted	AAM24513	22	957	9.5	488	
Human MUCII polype	AAY59288	21	957		\sim	
e #286	AAM04187	22	617		\sim	
1,582	AAM16458	22	617		48	
11 882	AAR26042	L U	826			
ortion of cryp	AAB11727	21	1721		489	
AP.	AAB50362	22	3118	9.5		
•	AAB50363	22	2972		89.	
Human ORFX ORF995	AAB41231	21	2971		496.5	
Cryptosporidium pa	AAB11726	21	1837		50	
н	AAP82975	9	744		6	
	AAY54466	21	788		20.	
acid	AAY54467	21	807	0	4	
ce of	AAP60570	7	844	0	54	
ortho	6056	22	472		578.5	
cterium	AAW31855	18	572	11.9	61	
e gi/10		21	4412	12.1		
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ALIGNMENTS

AAM24322 RESULT

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AAM24322 standard; Protein; 1299

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12-OCT-2001 (first entry)

AAM24322;

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DR P P I I
                                                         25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                       Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                Tang YT,
Cao Y, I
                                                                                                                      02-AUG-2001
                                                                                                                                        WO200154477-A2.
                                                                                                                                                                                                                   Human EST encoded protein SEQ ID NO: 1847.
WPI; 2001-476164/51
                                                                                                      25-JAN-2001; 2001WO-US02687
                                                                                                                                                        Homo sapiens.
                                          (HYSE-) HYSEQ INC
                Drmanac RA,
                                                          ; 2000US-0491404.
; 2000US-0617746.
; 2000US-0631451.
; 2000US-0663870.
              Zhou F, .
RA, Zhang
                 Qian
                   Werhman
                          XB,
                   Wang
an T;
                          Ζ,
                           Chen
                           72,
                            Asundi
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Matches 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11;
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antimycobacterial; antibiot;
                      458
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)B; AAT93610.
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93; Conservative
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Pred, No. 2.7e-27;
9; Mismatches 253;
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Best Local
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11-SEP-1984;
10-SEP-1985;
                                                                                                         The inventors claim a novel DNA molecule which comprises nucleotide sequence corresp. to all or a portion of the l sequence coding RESA (AAN60472) or FIRA (AAN60473). RESJ antigenicity suitable for providing protective immunity plasmodium falciparum malarial infections.
                                                                                            Sequence
                                                                                                                                                                       Disclosure; Fig 7;
                                                                                                                                                                                                DNA coding for Plasmodium falciparum antigens - poly:peptide(s) having antigenicity of RESA or F
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of (FIRA).
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                   ; gene therapy; protein 608; osteoporosis; bone density; gi/1017427/emb/CAA62189.
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WO9960164-A1 Unidentified

25-NOV-1999

14-MAY-1999; 99WO-US11066

15-MAY-1998; 98US-0085673

(QUAR-) QUARK BIOTECH INC

ď Mor 0, Skaliter R, Feinstein E Faerman A:

WPI;

identification of stress induced ger
preventing, treating or controlling preventing, treating genes for determining osteoporosis risk

Claim 32; Fig 6A-R; 308pp; English

identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular fractions and extracting mRNA from them, and differentially analysing the mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a madicament for contributions. after subjecting rat osteoblasts to mechanical stress. Expression of the 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain who expression of the following the subjected to mechanical strain who expectations in the method of the invention after the subjected to mechanical strain who expectations in the method of the invention after the subject to mechanical strain who expectations in the method of the invention after the subject to mechanical strain who expectation in the method of the invention after the subject to mechanical strains and the subject that the subject the subject to the subject to the subject that the subject the subject that the subject the subject that the The present sequence is obtained from a clustral X alignment with protein 608. Protein 608 was identified using the method of the in to mechanical strain. The specification describes a method for the controlling a physiological or disease state (especially osteoporosis or bone density or other factors causing or contributing to osteoporosis or its symptoms or other conditions involved in mechanical stress of its medicament for gene therapy. These medicaments, or genes identified the method of the invention, are used for treating, preventing or symptoms or other The methods can also be used for advancing research or osteoporosis or studies γď

RESULT 14 AAW31855

AAW31855 standard; Protein; 572

A

DEX DX ACX

27-APR-1998 AAW31855

(first entry)

Mycobacterium tuberculosis

55 kDa

protein

Sequence 4412 AA;

Query Match

11.5%; Score 625.5; DΒ 21; Length 4412;

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                                                                                                                                                                                                                                                                                                                  29-APR-1996;
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   ·Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) acts as a synovium lubricant, and can be used to lubricate tissue and joints in the treatment of osteoarthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence represents the bovine orthologue of human MSF, superficial zone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camprodactyly-arthropathy-coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous injection. The human CACP protein is identified in the invention as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1925-31, and mutations in this gene are responsible for the heritable disorder camptodactyly this gene are responsible for the heritable disorder camptodactyly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vara-pericarditis protein in combination with an anesthetic, useful for treating osteoarthritis, or as lubricants of tissue and joints \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (SZP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1;
                                                                                                                                                                                                                                                                                                09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                           AAM03645 standard;
                                                                                            29-JAN-2001;
                                                                                                                          09-AUG-2001.
                                                                                                                                                         WO200157270-A2
                                                                                                                                                                                                                    inflammatory
                                                                                                                                                                                                                                    Probe; human;
                                                                                                                                                                                                                                                               Peptide #2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       867
                                                                                                                                                                                                                                                                                                                                                                                                                                    254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               808 PKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRK-MTSTMPELNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEVWGIPSPIDTVFTRCNCEGKTFFFK 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt vrgpsqgfginpmfsdetnlcngrpvdglttlrngilvafrghyfwmltpftppppprrise}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s-lpeamlqtttrptptpnseiidvnsenedgdaaegekphmifrppvltpivipgteii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pkgratnsqvttpkpqkptkapkkptstkkprt-prvrkpkttptppktttsampeptpt
                                                                                                                                                                                                                                                                                                                                                                                                                                    tevwgipspidtvftrcncegktfffk 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                            2001WO-US00661
                                                                                                                                                                                                                     disease;
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                     breast disease;
                                                                                                                                                                                                                                                                  encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34pp;
                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.2%;
74.9%;
                                                                                                                                                                                                                    proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 823.5;
Pred. No. 2.
                                                                                                                                                                                                                                       breast
                                                                                                                                                                                                                                                                for measuring
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                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                       breast disease;
                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                   breast gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                       development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                        non-carcinoma
                                                                                                                                                                                                                                                                   expression
                                                                                                                                                                                                                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472;
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                                                                      QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by such probe. The probes are useful for measuring human gene expression a human breast sample, where the probe hybridises at high stringency to nucleic acid expressed in the human breast. The probes are useful for nucleic acid expressed in the human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel single exon nucleic acid probe used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast disease and non-carcinoma tumours.
Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                                           239
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                                                                                                                                                                                                                                                                                                                                                                                                                        179
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                                              533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tthkesagkkhitpapkskincrksttgkstvtrksdktgrpleksmstldktstsshkt 178
                                                                                                                                                                                                                                                                                            rertanentapf pagptenrem tanenttlf paeptehger tanenttps paeptehger \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-----KPINPRPSLPPN---SDTSKET-------
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KKLTPTTPEKLAPTTPEEKAAPTTPEEELAPTTPEEEPAPTTPKAAAPNT---PK
                                                                                                                                                                     {\tt enrertanenttpspagptenrettanekttlspveptenrettanekttpspaepteng}
                                                                                                                                                                                                    -TKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPA----PTTTKEPSPTTPKEPA---
                                                                                                                                                                                                                                                                 TTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTP----
                                                                                                                                                                                                                                                                                                                            TIKSA--PTTPKEPAPT-----
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                                                                                                                                                                                                                                                                                                                                                                                        PKAETTTKGPALT - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt ttsfhnsgnsqtkqkstsfpekitaaskttykttgtpeesektedsrttvasdklltktt}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nttrhskptdkptgnsktidhk-sstdnheapptseenssnggkdpmirngrsvdpadst 118
                                            engdrtplanekttpslaeptenggrtpfanekttsssaeptehee---rtplanenttp
                                                                           EPAPTTPKKPAPTTPKEPAPT----
                                                                                                        qrtpfanekttsssaeptehgertplanen-
                                                                                                                                                                                                                                  tane----nttpspaeptehgertpfandkttsssaestehgertplanenttpspaept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                        -----PTTTKSA-PTTTKEPAPTTTKSAPTTPKEPSPTTTKE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No 12385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast
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2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NKQTSTDGKEKTTSAKET---
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26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 771.5;
Pred. No. 6e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                         -TPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTP
                                                                                                                                                                                                                                                                                                                               -TTKSAPTTPKEPAPTTTKE---PAPTTPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                           -ttpspaeptenrertanekttpspaept
                                                                                                                                                                                                                                                                                                                                                                                         -TPKEPTPT---TPKEPASTTPKEPTPT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---QSIEKT-SAKDLAPTSKVLAKPT 133
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format
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                                                                                                                                           PAPTTPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                      479
                                                                                422
                                                                                                                                                                                                                                                                                                    358
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                                                                                                                532
                                                                                                                                                                           474
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ion in
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                                                   589
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Domain

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Multimeric protein, especially enzymatic, complexes are held together CC by protein protein interactions between domains designated dockerins and cohesins, which are found on the catalytic and scaffold subunits CC respectively. An example of such a complex is the cellulose degrading CC protein complex from Clostridium thermocellum, known as the celluloseme. CC interact with a central "scaffold" protein designated the cellulosome cC interact with a central "scaffold" protein designated the cellulosome cC interact with the Cip subunit via conserved 23 amino acid dockerin CC domains. Cip has been shown to contain 9 copies of a cohesin domain. CC domains. Cip has been shown to contain 9 copies of a cohesin domain. CC domain is designated a type II dockerin domain found on the catalytic subunits of the cellulosome. CC domain is designated a type II dockerin domain (as compared to the type II dockerin domain (as compared to the type CI is unable to bind type I cohesin domains. CC The sequence presented here is an example of a protein which binds the novel type II dockerin domains in the N-terminal portion of the OldB gene. CC The protein contains 4 type II cohesin domains in the N-terminal contains. The novel type II dockerin and is the product of the OldB gene. CC the novel type II dockerin and is the product so the voyable to bind type II dockerin and is the protein which binds combined type II dockerin and cohesin domains can be used in commisser. Pensentally ensure commisser and cohesin domains can be used commisser.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Pagé 31-39; 60pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellulase proteins with cohesin or dockerin type II domains - new potentiating the activity of multiprotein enzyme complexes
                                            302
                                                                                 865
                                                                                                                                                                                         187
                                                                                                                                                                                                                           758
                                                                                                                                                                                                                                                   128 VLAKPTP-KAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beguin
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               sdeptpsdeptps--deptps--deptp-sdeptpsetpeepiptdtpsdeptpsdeptp
sdeptpsdeptpsdeptpsetpeepiptdtpsdeptpsdeptps--
                                                                                                        KPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPT-TPKEPAPTAPKKPAPTTPKEPAP
                                                                                                                                          eptpsetpeepiptdtpsdeptpsdeptpsdeptpsdeptpsetpeepiptdtp
                                                                                                                                                                             TKSAPTTPKEPAPTTTKEPAPTTPKEPA----PTTTKEPAPTTTKSAPTTPKEPAPTTPK
                                                                                                                                                                                                                vviqpapikaasdepiptdtpsdeptps-----deptps---deptpsdeptpsd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-011569/02.
DB; AAT86623.
                                                                                                                                                                                                                                                                                                                                                                                                                            a synergistic manner
                                                                                                                                                                                                                                                                                                                                                                                           1664
                                                                                                                                                                                                                                                                                                                                                                                                                                          The novel type II dockerin and cohesin domains can s, especially enzyme complexes, to potentiate their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leibovitz
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                              17.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "cohesin type II domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme complexes, to potentiate their catalytic
                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                           Score 942; DB
Pred. No. 1.8e
83; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ι
                                                                                                                                                                                                                                                                                         DB 19;
1.8e-45;
hes 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain"
                                                                                                                                                                                                                                                                                                                              Length 1664;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                           166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful
                                                                       919
                                                                                                          301
                                                                                                                                                                                                                    804
                                                                                                                                            864
                                                                                                                                                                               242
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Ş В 8 밁

Š 밁

New composition comprising the camptodactyly-arthropathy-coxa

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RESULT 10
AAB60569
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                          WPI; 2001-182721/18
                                                                                                             23-JUL-1999;
19-JUL-2000;
                                                                                                                                                                                                                                                                      superficial zone protein; SZP; MSF osteoarthritis; joint lubrication;
                                                                                                                                                                                                                                                                                Bovine; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; superficial zone protein; SZP; MSF orthologue; synovial lubricant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1373
                                                                                   (UYCA-) UNIV
                                                                                                                                                        21-JUL-2000; 2000WO-US20002
                                                                                                                                                                                     01-FEB-2001
                                                                                                                                                                                                               WO200107068-A1.
                                                                                                                                                                                                                                                                                                                           Bovine MSF orthologue, superficial zone
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB60569 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 TKEPAPTTPKEPAPTTPKKPAPTTPKEPAPT-TPKEPAPTTTKKPAPTAPKEPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLP 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            setpeeptptttp----tptpsttptsgsggsggsggggggggtvptsptptpts---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ-KP 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eptpsdeptpsdeptpsdeptpsdeptpsdeptpsetpeepiptdtpsdeptps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psetpeep----iptdtpsdeptpsdeptpsdeptpsd-eptpsdeptpsetpeepipt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PT-TPKKPAPKELAPTTTKGPTSTTSDKPAPT---TPKETAPTTPKEPAPT-TPKKPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --kptstpapteie-eptpsdvpgaiggehraylrgy-----pdgsfrp 1465
                                                                                 CASE WESTERN RESERVE
                                                                                                             99US-0145328
2000US-0145328
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -eptpsde--ptpsdeptpsd----eptpsdeptpsetpeepiptdtpsdep
                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                     472
                                                                                                                                                                                                                                                                   orthologue; synovial lubric osteopathic; antiarthritic
                                                                                                                                                                                                                                                                                                                            protein (SZP).
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28-JUL-1999
02-AUG-1999
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04-AUG-1999
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-Sn66 -Sn66 -Sn66

S-0147260. S-0147303. S-0147416.

99US-0145386.
99US-0146388.
99US-0146389.
99US-0147038.
99US-0147204.
99US-0147302.
99US-0147192.

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FTT FTT XXX
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Best Local S
Matches 226
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                          Multimer; enzyme; complex; protein-protein interaction; dockerin domain; cohesin domain; catalytic subunit; scaffold subunit; SdDA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.
                                                                                                                                             C. thermocellum OlpB protein.
                                                                                                                                                                     16-OCT-1998
                                                                                                                                                                                           AAW43106;
                                                                                                                                                                                                                     AAW43106
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                                                                      Clostridium
                                                Key
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            Domain
                                     Domain
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                                                                                                                                                                                                                                                                                                    P---TTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKP 710
                                                                                                                                                                                                                                                                                                                            lppntppqipptlppntppqtppntppetppntppqtpptvppntppvtppvrppttpps
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                                                                                                                                                                                                                     standard; Protein; 1664
                                                                        thermocellum
                                                                                                                                                                     (first entry)
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99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
          Location/Qualifiers 28..192
/note= "cohesin type 207..363"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%;
  "cohesin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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Pred. No. 5.1e-48;
4; Mismatches 293
                         type
                                                                                                                                                                                                                       A
   II domain'
                          II domain"
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                                                                                                                                                                                                                                                                                   681
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10-SEP-1999; 13-SEP-1999; 15-SEP-1999; 16-SEP-1999;

990S-0147493
990S-0148171
990S-0148319
990S-0148341
990S-0148565
990S-0149426
990S-0149426
990S-0149723
990S-0149929
990S-0150566
990S-0150566
990S-0151086
990S-0151086
990S-0151086
990S-0151086
990S-0151333
990S-015428
990S-015428
990S-015428
990S-0155556
990S-015578
990S-015428
990S-015428
990S-015565
990S-015565
990S-015565
990S-015565
990S-015775
990S-0158029
990S-0159294
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990S-0159330
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990S-0159331

20-SEP-1999 22-SEP-1999 23-SEP-1999 24-SEP-1999 24-SEP-1999 26-SEP-1999 06-CCT-1999 06-CCT-1999 07-CCT-1999 11-CCT-1999 11-CCT-1999

990S-0159584 990S-0160741 990S-0160767 990S-0160768 990S-0160814 990S-0160814 990S-0160815 990S-0160980 990S-0160981 990S-0160981 990S-0161404 990S-0161404 990S-0161406 990S-0161405 990S-0161405 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999;

18-AUG-1999;

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RESULT
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                25-FEB-1999

05-MAR 1999

23-MAR 1999

25-MAR 1999

25-MAR 1999

25-MAR 1999

01-APR-1999

01-APR-1999

01-APR-1999

16-APR-1999

17-APR-1999

21-APR-1999

23-APR-1999

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15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
                  (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the patients of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its
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genic; gene therapy; vaccine; colonic cancer.
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polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AA128460 to AA1285 g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 AAM24494 to AAM24523 represent nucleotide and amino acid sequences the exemplification of the present invention

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Pred. No. 2.7e-174;
8; Mismatches 80; I
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Query Match 25.1 Best Local Similarity 88.3 Matches 263; Conservative

25.1%;

Score 1357.5; DB 16; Pred. No. 1.6e-69; 3; Mismatches 21;

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This sequence represents the human megakaryocytopolentin (MPO) protein. This sequence was purified using a carrier which can couple wheat germ agglutinin and heparin to separate MPO. Fragments of this sequence (see ARR0039 and AAR80049) were used to produce the amplification primers can then be used as probes to screen human cDNA libraries for MPO cDNA can then be inserted into a plasmid which is used to transform cells to produce MPO. The MPO sequence is capable of promoting colony formation of megakaryocytes, enlarging the size of megakaryocytes factor may be used for treating thrombocytopenia and hematocytopenia. The purification method can be used to isolate MPO from human urine or serums of patients with aplastic anaemia, and from animal blood or urine the pradiation exposing the animals to induce aplastic anaemia.
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452 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indicates the presence of or predisposition to developing in the osteoarthritis. The tribonectin and DNA encoding it are useful in the osteoarthritis. The tribonectin and DNA encoding it are useful in the treatment of osteoarthritis, where they may be used for lubricating treatment of osteoarthritis, where they may be used for lubricating the tribonectin, when formulated as a membrane, foam, gel or fibre, is the tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic;
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                                                                                            of diagnosing osteoarthritis or a predisposition to osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a mammal, wherein an increased amount of MSF compared to a control indicates the presence of or predisposition to developing it research that tribonectin and DNA encoding it are useful in the osteoarthritis. The tribonectin and DNA encoding it are useful in the reatment of osteoarthritis, where they may be used for lubricating mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is the interest of the second of the
                                                                                                                                                                                                                                                                                             The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one o-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT repeats of a motif having at least 50% identity to the sequence KEPAPTT repeats of a motif having at least 50% identity to the sequence comprising a (AAB29774). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin, a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of diagnosing osteoarthritis or a predisposition to osteoarthritis by
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useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant To
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Page -;

English

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The invention relates to a method of treating osteoarthritis via the Cadministration of a composition comprising the camptodactyly-arthropathy-cox vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may be administered via intra-articular or intravenous of the invention may be administered via intra-articular or intravenous confidence in the human CACP protein is identified in the invention as their gene estimulating factor (MSF). The gene encoding confidence in (MSF) is located on chromosome 1925-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-carthropathy-coxa vara-pericarditis, in which patients have synovial contents as a synoviam lubricant, and can be used to lubricate tissue and contents in the treatment of osteoarthritis. The composition may be content in the treatment of osteoarthritis (e.g., joint pain, contents in the treatment of osteoarthritis (e.g., joint pain, contents in the treatment of osteoarthritis (e.g., joint pain, contents in the treatment of osteoarthritis (e.g., joint pain, contents in the treatment of osteoarthritis (e.g., joint pain, contents in the sequence is not given in its entirety in figure 4 of the contents and content
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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating molety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of diagnosing osteoarthritis or a predisposition to osteoarthritis by
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MSF; megakaryocyte stimulating factor; tribonectin; alternative splicing; joint boundary lubricant; 0-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic;
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N-PSDB; AAC81498.
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cc time sequence given is a full length translation from the meghanization of stimulating factor (MSF) precursor. The sequence covered by exons II, and IV encodes megakaryocyte stimulating factor (MSF). This cc sequence is modified by the addition of an N-terminal sequence encoding cc a secretory leader, an initiating methionine proceeding exon II and a cc terminating codon following exon IV. The cDNA sequence given contains cc (meg-CSF). Exon I contains the initiating methionine, and encodes a cc classical mammalian protein secretion signal sequence. The sequence cc encoding the original meg-CSF includes exons II-IV and is thought to cc primary transcript of this gene may be cleaved in different ways to cyleid a family of mRNA's each encoding a different ways to cyleid a family of mRNA's each encoding a different ways to combinate in the stability, folding and processing of the care also implicated in the stability, folding and processing of the considerated in the processing or folding and processing of the resulting factor, ie. one or more of these exons may contain cc the resulting factor, ie. one or more of these exons may contain cc the cellular matrix or extracellular matrix processing. Both naturally occuring and non-naturally occuring was processing. Both naturally combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different contains.
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DB; AAQ27223.
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\verb|pttpkepaptttkepspttpkepaptttksaptttkepaptttksapttpkepsptttke|
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                                                                                                                                                                                                                                                                                                                                                                                             1404 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 5416; DB 13; 100.0%; Pred. No. 2.6e-298; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating or drugs,
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New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint

useful

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2000US-0145328
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Query Match
Best Local Similarity
Matches 1013; Conserv
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 TERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTT
                                       \verb|kelaptttkgptsttsdkpapttpketapttpkepapttpkkpapttpetpppttsevst|
                                                                                                          KELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVST
                                                                                                                                               eptsttsdkpapttpkgtapttpkepapttpkepapttpkgtapttlkepapttpkkpap
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                                                                                                                                                                                                                  PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
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18-JAN-1991;
10-SEP-1991;
                        (GEMY ) GENETICS INST INC
                                                                                                       06-AUG-1992
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  Gesner
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C899P predicted am
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Human ORFX ORF2255	AAB42491	21	3266	7.9		5
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# 90 /		22	2665	7.9	428.5	3
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Peptide #128 end		22	511	8.6	467.5	34
Peptide #1349 end	AAM27312	22	511	8.6	σ	ũ
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Human SRCAP. Homo		22	2972	9.0	489.5	_ (
Human ORFX ORF995		21	2971	9.2	496.5	0
Bioadhesive precur		9	744	9.4	506.5	9
ъ.		21	1837	9.4	508	Φ.
Amino acid sequenc	AAY54466	21	788	9.6	520.5	7
		21	807	10.0	542	20
	~	7	844	10.0	544	U
Mycobacterium cube		18	572	11.3		4
Sequence g1/101/42		21	4412	11.5	625.5	ω
Mycobacterium tube	AAW31852	18	763	13.2	715	N

ALIGNMENTS

AAM24322 ID AAM2

AAM24322 standard;

Protein; 1299

AAM24322;

Human EST encoded protein SEQ ID NO: 1847.

12-OCT-2001 (first entry)

RESULT

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25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder;
                                                                                                                                                                                       biodiversity; gene therapy; nutrition
WPI; 2001-476164/51
                 Tang YT, Liu C, Z
Cao Y, Drmanac RA,
                                                                                                                25-JAN-2001; 2001WO-US02687
                                                                                                                                  02-AUG-2001.
                                                                                                                                                     WO200154477-A2.
                                                                                                                                                                       Homo sapiens
                                             (HYSE-) HYSEQ INC
                   Zhou P,
A, Zhang
                   Qian XB,
J, Werhm
                     xB, Wang
Werhman T;
                              Ζ,
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Matches 243
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11-SEP-1984;
10-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA and FIRA antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA coding for Plasmodium falciparum antigens - expressing poly:peptide(s) having antigenicity of RESA or FIRA antigens falciparum
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N-PSDB; AAN60473.
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RESULT
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                   This novel 55 kba protein is encoded by an open reading frame of a Mycobacterium tuberculosis DNA fragment (see AAT93610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAM31851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacteria.
     claimed
                                                                                                                                             Claim 11; Fig 16; 55pp; English
                                                                                                                                                                     New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
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Best Local :
                    W08601802-A
                                           Plasmodium falciparum
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                                                                    Malaria
                                                                                                        Sequence of
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                                                                                                                                                                          Mechanical stress; gene therapy; protein 608; osteoporosis; bone development; gi/1017427/emb/CAA62189.
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Sequence

4412 AA;

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An An An An An An Annalysis of the present sequence is obtained from a clustral X alignment with CC protein 608. Protein 608 was identified using the method of the invention CC after subjecting rat osteoblasts to mechanical stress. Expression of the CC 608 gene was found to be upregulated by about 3-fold in cells subjected CC identification of genes responsive to a specific mechanical stress. The CC identification of genes responsive to a specific mechanical stress. The CC identification of genes responsive to a specific cellular stress. The CC identification and extracting mRNA from them, and differentially analysing the fractions and extracting mRNA from them, and differentially analysing the CC genes whose expression is responsive to a specific stress. The identified CC genes are employed in determining risk associated with a physiological or CC disease state. The risk determination methods are used for testing a CC medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating preventing or controlling a physiological or disease state (especially osteoporosis or its symptoms or other conditions involved in mechanical stress or its symptoms or other conditions involved in mechanical stress or its control. The methods can also be used for advancing research or studies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 32; Fig 6A-R; 308pp; English.
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                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
                                                                                                                                                                                                                                                                            anti-mycobacterial drugs
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Conservative

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27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                       The present invention relates to novel single exon nucleic acid probes (see AAI0001-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
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                                                                                                  breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                          Claim 27;
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2000US-0608408.
2000US-0632366.
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disease; proliferative breast di
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Score 771.5; DB 22
Pred. No. 3.7e-36;
7; Mismatches 466;
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29-SEP-1999;
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99US-0160767.
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38.5%;
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Pred. No. 2.6e
24; Mismatches
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2.6e-48;
hes 293;
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                                                                                                                                                                 Cellulase proteins with cohesin or dockerin type II domains for potentiating the activity of multiprotein enzyme complex
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                                                                                                                                                                                                                                                                                                                                                                                                                              domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                enzyme; complex; protein-protein interaction; dockerin domain;
omain; catalytic subunit; scaffold subunit; SdbA; synergistic;
me integrating protein; scaffoldin dockerin binding protein.
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interact with a central "scaffold" protein designated the cellulosome integrating protein (CipA; see AAW43108). The catalytic subunits interact with the Cip subunit via conserved 23 amino acid dockerin domains. Cip has been shown to contain 9 copies of a cohesin domain. The invention relates to the isolation of proteins binding to a novel dockerin type domain found in the C-terminal portion of Cip. The new domain is designated a type II dockerin domain (as compared to the type I domain found on the catalytic subunits of the cellulosome). The type II dockerin domain domain has some sequence similarity to the type I dockerins unable to bind type I cohesin domain. Multimeric protein, especially enzymatic, complexes are held together by protein-protein interactions between domains designated dockerins and cohesins, which are found on the catalytic and scaffold subunits respectively. An example of such a complex is the cellulose degrading protein complex from Clostridium thermocellum, known as the cellulosome. This complex comprises around 15 proteins including endoglucanases, cellobiohydratases, hemicellulases, e.g. xylanases or lichinases, which interact with a central "scaffold" protein designated the cellulosome sequence presented example O. a protein which binds

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coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.
The composition may further comprise a local anaesthetic. The composition
of the invention may be administered via intra-articular or intravenous
confidence of the invention may be administered via intra-articular or intravenous
confidence of the invention may be administered via intra-articular or intravenous
confidence of the invention may be administered via intra-articular or intravenous
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confidence of the intra-articular or intravenous
confidence of inflammation. CACP protein (MSF)
confidence of inflammation. CACP protein (MSF)
confidence of intravenous of costeoarthritis. The composition may be
applied to reduce the symptoms of osteoarthritis. The composition may be
confidence of movement or joint damage). The present sequence
represents the bovine orthologue of human MSF, superficial zone
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Best Local Similarity
Matches 197; Conser
                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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06-SEP-2000 EP1033405-A2

WPI; 2001-441847/47

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RESULT
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Best Local
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                                                                                                      30-DEC-1999;
10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                        C899P predicted
                                                                                                                                                                                                                                                                                                   Human; immunotherapy; diagnosis; colon cancer; colon tumour;
immunogenic; gene therapy; vaccine; colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              AAM24516;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAM24516 standard;
                        Xu J,
                                                                                                                                                                                         29-DEC-2000; 2000WO-US35596
                                                                                                                                                                                                                    12-JUL-2001
                                                                                                                                                                                                                                               WO200149716-A2
                                                                                                                                                                                                                                                                                                  immunogenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPIN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dlaptskvlakptpkaetttkgpalttpkeptpttpkepasttpkeptpttiksapttpk 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLAPTSKVLAKPTPKAETTTKGPALLTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctqp-----tpkephpplprslhpptkepapttpkepaptapkkpaplpple 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT 240
            Lodes MJ,
E, Wang T,
                                                    CORIXA CORP
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                                                                            2000US-0480321.
2000US-0504629.
2000US-0519444.
2000US-0575251.
2000US-0609448.
2000US-0649811.
                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                99US-0476296
                                                                                                                                                                                                                                                                                                                                           amino
            Secrist H,
Jiang Y;
                                                                                                                                                                                                                                                                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                                                                                                                                                                                                                                           acid
                                                                                                                                                                                                                                                                                                                                          sequence
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Pred. No. 5.9e-70;
3; Mismatches 21; I
                            Benson
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                            DR,
                            Meagher
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The present invention describes colon tumour associated proteins (I) and CC (II) and (II) can be used in gene therapy and vaccine production. (I) and CC (II) may be used in the prevention, diagnosts and treatment of diseases CC associated with inappropriate colon tumour associated protein (TCAP) CC expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by CC expression, such as colonic cancer. For example, (I) and (II) may be CC used to treat disorders associated with decreased expression by CC excitivity of TCAPs by expressing inactive proteins or to supplement the CC patients own production of them. Additionally, (II) may be used to CC produce the TCAP proteins, by inserting the nucleic acids into a host CC complementary sequences may also be used as DNA probes in diagnostic CC complementary sequences may also be used as DNA probes in diagnostic CC quantitate the presence of similar nucleic acids in samples, and CC quantitate the presence of similar nucleic acids in samples, and CC also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used to down regulate CC as diagnostic agents for detecting the presence of TCAPs in samples as diagnostic agents for detecting the presence of TCAPs in samples to the production of antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples to the production as a diagnostic agents for detecting the presence of TCAPs in samples to the presence of TCAPs in the presence of TCAPs in the presence of 
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                                                                                                               (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 446-462; 472pp; English
                                                                              the exemplification of the present invention
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Best Local S
Matches 363
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                                                                                                                  ittttppptttpsppttttttppptttpspptttpitpptstttlpptttpspppttttt 1650
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                                                                                                                                                                                                                                                                                                                                                  KEPT----PTTPKEPASTTPKEPTPTTTKSAP-TTPKEP-----APTTTKSAP-TTP 194
                                                                                                                                                                                                                                                                                                                                                                                                                       ETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTP 148
                        tttttpsstttpspppttmttpsptttpspptttmttlpptttsspltttplppsitppt 1769
                                                            ТТТКЕРАРТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРАРТТТККРАРТАРКЕРАРТТР- 414
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-KKLTP 427
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QΥ

20

Qy

Qy

QΥ

Sequence

5179 AA;

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CC lubricating molety and has a polypeptide sequence comprising 1-76
CC repeats of a motif having at least 50% identity to the sequence KEPAPTT
CC (AAB29774). The invention also relates to a nucleic acid encoding a
CC human MSF-derived tribonectin; a biocompatible composition comprising a
CC human tribonectin for inhibiting tissue adhesion formation; and a method
CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by
CC measuring the amount of MSF or its fragment in a biological sample of a
CC indicates the presence of or predisposition to developing
CC osteoarthritis. The tribonectin and DNA encoding it are useful in the
CC treatment of osteoarthritis, where they may be used for lubricating
CC mammalian joints, such as articulating joints of humans, dogs or horses.
CC The tribonectin, when formulated as a membrane, foam, gel or fibre, is
CC useful for inhibiting adhesion between two surfaces such as the injured
CC tissues of a mammal, where the injury is caused by a surgical insertion
CC or trauma, or an artificial device e.g., an orthopaedic implant. In
CC particular, one of the surfaces is pericardial tissue. DNA encoding a
CC tribonectin may be used in gene therapy. The present sequence represents
CC a substantial portion of a human MSF-derived tribonectin.
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Best Local Similarity
Matches 794; Conserv
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                                                                                          KELAPTITKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVST
                                                                                                                                                                         EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAP
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Pred. No. 1.4e-190;
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õ 망 õ 문 Q 밁 õ 밁 Ş 밁 ş В δÃ 밁 Ş 용 á В Š g 8 밁

This sequence represents the human megakaryocytopoientin (MPO) prote This sequence was purified using a carrier which can couple wheat get agglutinin and heparin to separate MPO. Fragments of this sequence AAR80039 and AAR80040) were used to produce the amplification primes

protein.

(see

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RESULT
AARR800A1
ID AARR80A2
XX AARR8
XX AARR8
XX Huma
XX Huma
XX Huma
XX Huma
XX Mey
FT M1sc

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                                                                                                           Example;
                                                                                                                                                                                                                       WPI; 1995-320576/41.
N-PSDB; AAT04546.
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The invention relates to a human tribonectin which is a product of calternative splicing of the human MSF (megakaryocyte stimulating factor) cg gene. The tribonectin has at least one O-linked oligosaccharide clubricating molety and has a polypeptide sequence comprising 1-76 (AAB29774). The invention also relates to a nucleic acid encoding a cc human MSF derived tribonectin; a biocompatible composition comprising a cc human tribonectin for inhibiting tissue adhesion formation; and a method co f diagnosing osteoarthritis or a predisposition to osteoarthritis by cmeasuring the amount of MSF or its fragment in a biological sample of a mammal, wherein an increased amount of MSF compared to a control costeoarthritis. The tribonectin and DNA encoding it are useful in the creatment of osteoarthritis, where they may be used for lubricating commammalian joints, such as articulating joints of humans, dogs or horses. Cc useful for inhibiting adhesion between two surfaces such as the injured ctissues of a mammal, where the injury is caused by a surgical insertion cor trauma, or an artificial device e.g., an orthopaedic implant. In cc uniman tribonectin may be used in gene therapy. The present sequence represents
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Matches 1064;
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                                                                                                                                                                   Novel tribonectin polypeptide useful as lubricant for osteoarthritis, comprises O-linked lubricating moiety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         administration of a composition comprising the camptodactyly-arthropathy-
CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.
CC The composition may further comprise a local anaesthetic. The composition
CC of the invention may be administered via intra-articular or intravenous
CC injection. The human CACP protein is identified in the invention as
CC cox protein (MSF) is located on chromosome 1925-31, and mutations in
CC chis gene are responsible for the heritable disorder camptodactyly-
CC arthropathy-coxa vara-pericarditis, in which patients have synovial
CC hyperplasia without evidence of inflammation. CACP protein (MSF)
CC acts as a synovium lubricant, and can be used to lubricate tissue and
CC oplied to reduce the symptoms of osteoarthritis. The composition may be
CC applied to reduce the symptoms of osteoarthritis (e.g., joint pain,
CC closs of range of movement or joint damage). The present sequence
CC Note: This sequence is not given in its entirety in figure 4 of the
CC sequence was therefore obtained from GenBank (U70316).
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Best Local Sim
Matches 1064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising the camptodactyly-arthropathy-coxavara-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint.
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                                                                                                                          PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPT
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                                                                                                                                                                                          Homo
                                                                                                                                                                                                                   Human MSF; megakaryocyte stimulating factor; talternative splicing; joint boundary lubricant osteoarthritis; tribosupplementation; tissue a friction coefficient reduction; gene therapy;
                              N-PSDB;
                              WPI; 2001-024673/03
N-PSDB; AAC81498.
                                                                                 (RHOD-)
                                                                                                       23-APR-1999;
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                                                                                                                                                                                                                 factor; tribonectin;
lubricant; O-linked oligosaccharide;
; tissue adhesion inhibition;
therapy; antiarthritic;
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Novel tribonectin polypeptide useful as lubricant osteoarthritis, comprises O-linked lubricating moi

moiety

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cc stimulating factor (MSP) precursor. The sequence covered by exons II, crim and IV encodes megakaryocyte stimulating factor (MSF). This criminating codon following exon IV. The colony stimulating factor (MSF). This criminating codon following exon IV. The colony stimulating factor (MSF). This criminating codon following exon IV. The colony stimulating factor (MSF). Exon I contains the initiating methionine proceeding exon II and a criminate in the region between amino acid residues 134 - 147. The colony transcript of this gene may be cleaved in different ways to criminaty transcript of this gene may be cleaved in different tays to criminaty transcript of this gene may be cleaved in different tays to compare also implicated in the stability, folding and processing of the synergy of MSF with other cytokines. Exons V - XII are believed to be implicated in the processing or folding of the appropriate structure of the cellular matrix or extracellular matrix processing. Sequence of the cellular matrix or extracellular matrix processing. Set the cocuring and non-naturally occuring MSF's may be characterised by various combinations of alternatively spliced exons from this sequence. The members of the MSF family.
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                                                         PTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE
                                                                                          \verb|pkkpapttpkepapttpkeptpttpkepapttkepapttpkepaptapkkpapttpkepa|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 and 3; Fig 1; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gesner TG,
                                                                                                                                                                                                                                                                                                                                                                                           1404 AA
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is a full length translation from the megakaryocyte (MSF) precursor. The semence
                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                  score 5698;
Pred. No. 0;
0; Mismatches
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e to radiation
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or drugs,
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                           Length 1404;
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                                                                                                                                                             Human; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; MSF; megakaryocyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
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23-JUL-1999;
19-JUL-2000;
                                        21-JUL-2000;
                                                                 01-FEB-2001
                                                                                                                        Homo sapiens
                                                                                                                                                   antiarthritic.
                                                                                                                                                                                                                   Human megakaryocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \verb|mprvrkp| kttptprkmtstmpelnptsriaeamlqtttrpnqtpnsklvevnpksedagg|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aegetphmllrphvfmpevtpdmdylprvpnqgiiinpmlsdetnicngkpvdglttlrn\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRN
                                                                                                                                                                                                                                                                                                      standard;
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 99US-0145328
2000US-0145328
                                        2000WO-US20002
                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                      stimulating
                                                                                                                                                                                                                                                 entry)
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(UYCA-) UNIV CASE WESTERN RESERVE

Claim

20;

Sequence

1039

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Query Match 100.
Best Local Similarity 100.
Matches 1064; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) forensics, gene mapping, identification of mutations, to assess blodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for treatment of diseases, antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH98981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TERDLATTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTT
                                                                                      kelaptttkgptsttsdkpapttpketapttpkepapttpkkpapttpetpppttsevst
                                                                                                    KELAPTTIKGPTSTTSDKPAPTIPKETAPTIPKEPAPTIPKKPAPTIPETPPPTTSEVST
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                                                                                                                                                    EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention.
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Pred. No. 0;
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RESULT
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10-SEP-1991;
                                              17-JAN-1992;
                                                                        06-AUG-1992
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91US-0757022.
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1373..14
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1331..13
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157..200
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107..157
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67..107
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.1331
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adhesion; alternative splicing.
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition. 25-JAN-2000; 2000US-0491404. 17-JUL-2000; 2000US-0617746. 03-AUG-2000; 2000US-0631451. 15-SEP-2000; 2000US-0663870. 25-JAN-2001; 2001WO-US02687 02-AUG-2001. WO200154477-A2 Homo sapiens

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The precursor CDNA sequence contains sequences derived from human CC megakarycoyte colony stimulating factor (meg-CSF). Exon I contains CC the initiating methionine, and encodes a classical mammalian protein CC secretion signal sequence. The sequence encoding the original meg-CSF CC includes exons II-IV and is thought to terminate in the region between CC amino acid residues 134 - 147. The primary transcript of this gene CC encoding a different ways to yield a family of mRNA's each CC encoding a different WSF protein. Exons V and VI are thought to be CC related to the activity of the factor and are also implicated in the CC stability, folding and processing of the molecule. These exons are CC cytokines. Exons V - XII are believed to be implicated in the CC processing or folding of the appropriate structure of MSF with other CC factor, i.e. one or more of these exons may contain sequences which CC direct proteolytic cleavage, adhesion, organisation of the cellular matrix or extracellular matrix processing. Both naturally occuring CC and non-naturally occuring MSF's may be characterised by various
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                                                                                                                                                                                                                                                The sequence covered by exons II, III and IV encodes megakaryocyte stimulating factor (MSF). This sequence was used to produce MSF as a fusion protein with thioredoxin. This sequence was derived from MSF-precursor (see also AAR26050).
                                                                                                                                                                                                                                                                                                                                                New human mega-karyocyte stimulating immune deficiencies, cancer, exposure bacterial and viral infections, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark SC,
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10-SEP-1991;
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DB; AAQ27224.
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proteolytic cleavage;
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91US-0757022
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, monitoring vaccination, and for the development of vaccines and
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Pred. No. 3.1e-31;
9; Mismatches 361;
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Query Match
Best Local Similarity
Matches 271; Conserv

Conservative

8.7%; Score 645.5; DB: 24.0%; Pred. No. 1.3e-26 tive 128; Mismatches 488

DB 21; 488;

Indels Length 4412;

243;

Gaps

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The present sequence is obtained from a clustral X alignment with CC protain 608. Protein 608 was identified using the method of the invention After subjecting rat osteoplasts to mechanical stress. Expression of the CC after subjecting rat osteoplasts to mechanical stress. Expression of the CC identification of genes responsive to a specific method for the CC identification of genes responsive to a specific mechanical stress. The CC method comprises applying the mechanical stress to an organism (tissue CC crells comprising bone cells), isolating the specific cellular CC fractions and extracting mRNA from them, and differentially analysing the CC mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identified CC genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or CC disease state. The risk determination methods are used for testing a controlling a physiological or disease state (especially osteoporosis or CC controlling a physiological or disease state (especially osteoporosis or CC its symptoms or other conditions involved in mechanical stress or its conditions involved in mechanical
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RESULT TARABLOR72 ID AARLOR72 ID AAR XX XX AARLOR72 Project AAR XX Megg EXX Megg EXX
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   29-JUN-1990;
08-AUG-1989;
28-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                      Megakaryocyte colony bleeding disorder.
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                                                                                                                        07-AUG-1990;
                                                                                                                                                                                 21-FEB-1991
                                                                                                                                                                                                                                       WO9102001-A
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by meg-CSF cDNA clone
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   90US-0546114.
89US-0390901.
89US-0457196.
                                                                                                                           90WO-US04421
                                                                                                                                                                                                                                                                                                                                                                                    stimulating
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                                                                                                                                                                                                                                                                                                                                                                                       platelet deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --KTTTLAPKVTTT------
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                                                                                                                                                                                                                                                                                                             ΧIJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 131; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The clone was isolated from a human placenta lambda phage DNA library. The sequence can be inserted into expression vectors the prodn. of recombinant meg-CSF. The protein is used to tre bleeding disorders and platelet deficiencies. See also AAR11372, AAR10870 and AAR10871.
                                                                                                                                                                                                                          antimycobacterial;
                                                                                                                                                                                                                                     Tuberculosis;
                                                                                                                                                                                                                                                                                                                      AAW31852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 85; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mega:karyocyte colony stimulating factor protein - regulates human haematopoiesis by stimulating growth and development of mega:karyocyte(s) in treatment of e.g. plastic anaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-073490/10.
N-PSDB; AAQ10582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gesner TG,
New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
                                                                                                                                                                                                                                                                              27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENETICS INST
                                                                                                                                                             06-NOV-1997
                                                                                                                                                                                  W09741252-A2
                                                                                                                                                                                                      Mycobacterium
                                                                                                                                                                                                                                                         Mycobacterium
                                             N-PSDB; AAT93610
                                                                                                                      29-APR-1996;
                                                                                                                                         18-APR-1997;
                                                       WPI; 1997-549750/50
                                                                                              (GBFB ) GBF
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                                                                                                                                                                                                                                                                                                                                                                                                                 cdaqckkydkccpdyesfcaevhnptsppsskkapppsgasqtiksttkrspkppnkkkt 152
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                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                GES BIOTECH
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                                                                                                                                                                                                                                     mycobacteria;
                                                                                                                                                                                                                                                          tuberculosis 74 kDa protein.
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                                                                                                                                           97WO-EP01973
                                                                                                                                                                                                                            antibiotic;
                                                                                                                                                                                                                                                                                                                        Protein;
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95.6%;
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                                                                             Moreno
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                                                                                                                                                                                                                                     infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 752; DB 12;
Pred. NO. 6.2e-34;
3; Mismatches 3
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                                                                                                  GMBH.
                                                                             Singh
                                                                                                                                                                                                                                      diagnosis;
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                          Probe: human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma
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2000US-0180312.
2000US-0207456.
2000US-0608408.
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Matches Query Match Best Local

cal Similarity
317; Conserv

10.9%; Score 805; DB 22; 26.2%; Pred. No. 7.2e-36;

Length 1325;

517;

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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, prollferative
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21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
                        breast disease and non-carcinoma tumours.

Note: The sequence data for this pateent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
Sequence
                                                                                                                                                                                                                                                                       Claim 27;
                                                                                                                                                                                                                                                                                                     Novel single exon nucleic acid probe used in a human breast -  \\
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-476286/51
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                                                                                                                                                                                                                                                                     SEQ ID No 12385;
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1325 AA;
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; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                322pp; English
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                                          part of the printed directly from WIPO
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pspaeptenrertanekttpspaeptengdrtplanekttpslaept---enggrtpfan
                                                                                                                                    ----PT----TTKSAPTTPKEPAPT-----TPKKPAPTTPKEPAPTTPKEPTP-----TT
                                            PKEPAPT-TKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEP
                                                                                                                                                                                saestehgertplanen--ttpspaeptenrertanenttpspagptenrettanekttl 446
                                                                                                                                                                                                                               SAPTTPK-EPAPTTTKSAPTTPKEPAPTTTKE-----PAPTTPKEPAPTTTKEPA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSTIWKIKSSKNS 164
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                                                                                          spveptenrettanekttpspaeptenggrtpfanekttsssaeptehgertplanentt
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29-OCT-1999;
                                                                                                                                                         Multimer; enzyme; complex; protein-protein interaction; dockerin domain; cohesin domain; catalytic subunit; scaffold subunit; SdbA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.
                                                                                                                                                                                                               C. thermocellum OlpB protein
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/note= "cohesin type
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303 VLAKPTP-KAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTT 361

Matches Query Match Best Local :

Local Similarity

Conservative

12.8%; 31.0%; 104;

Score 950; DB 19; Pred. No. 1.2e-43; 4; Mismatches 361

361;

55;

Length 1664; Indels 230;

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cc and cohesins, which are found on the cattalytic and scaffold subunits or protein complex from Clostridium thermocellum, known as the cellulosome. The complex is complex is complex is complex is complex in collulosome. This complex comprises around 15 proteins including endoglucanases, cellubiohydratases, hemicellulases, e.g. xylanases or lichinases, which cellubiohydratases, hemicellulases, e.g. xylanases or lichinases, which celluborated with a central "scaffold" protein designated the cellulosome integrating protein (Clph, see AAW43108). The catalytic subunits of interact with the cip subunit via conserved 23 amino acid dockerin commains. Cip has been shown to contain 9 copies of a cohesin domain. The invention relates to the isolation of proteins binding to a novel dockerin type domain found in the C-terminal portion of Cip. The new compared to the catalytic subunits of the cellulosome). The type I dockerin domain has some sequence similarity to the type I dockerins
                                     II dockerin domain has some sequence similarity to the type I dockerins but is unable to bind type I cohesin domains. The sequence presented here is an example of a protein which binds the novel type II dockerin domain and is the product of the OlpB gene. The protein contains 4 type II cohesin domains in the N-terminal portion of which the first domain (amino acid residues 28-192) is thought to bind CipA. The novel type II dockerin and cohesin domains can be used in complexes, especially enzyme complexes, to potentiate their catalytic actions in a synergistic manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multimeric protein, especially enzymatic, complexes are held together by protein-protein interactions between domains designated dockerins
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scscdtggdcecfcsavasyaqectkegac---
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                                                                                                                                                                                                                                                                                                                                                                                                       \verb|ptttpsspi-tttttpsstttpspppttmttpspttttpspptttmttlpptttssplttt|\\
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STPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEP-
                                          ttpitttttvtptptptgtqtptttpittttttvtptptptgtqtpt-ttpitttttvtpt
                                                                                                                                  EPTSTTSDKPAP-TTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA
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                                                                                                                                                                                                                                                     TTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPT-TPEEPAPTTPKAAAPNTPKEPAPTTP
                                                                                                                                                                                                                                                                                    \verb|niscratmypdvpigqlgqtvvcdvsvglicknedqkpggvipmafclnyeinvqccecv|
                                                                                                                                                                                                                                                                                                                     ----KKLTP------
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                                                                   PKELAPTITKGPTSTTSDKPAP-TTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEV
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                    -GVPT-TKTPAA 882
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                                                                                                                                                                                                                                                                                                                                                                                                              protein identification; signal transduction pathway; n
hybridisation assay; genetic mapping; gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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  990S-0132863.
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990S-0134221.
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990S-0134741.
990S-0135124.
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on control;
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promoter;
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CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.

CC of the composition may further comprise a local anaesthetic. The composition

CC of the invention may be administered via intra-articular or intravenous

CC injection. The human CACP protein is identified in the invention as

CC cacp grotein (MSF) is located on chromosome 1925-31, and mutations in

CC cacp protein (MSF) is located on chromosome 1925-31, and mutations in

CC cacp protein (MSF) is located on chromosome 1925-31, and mutations in

CC this gene are responsible for the heritable disorder camptodactyly-

CC arthropathy-coxa vara-pericarditis, in which patients have synovial

CC hyperplasia without evidence of inflammation. CACP protein (MSF)

CC acts as a synovium lubricant, and can be used to lubricate tissue and

CC applied to reduce the symptoms of osteoarthritis. The composition may be

CC applied to reduce the symptoms of osteoarthritis (e.g., joint pain,

CC capterpassa the bovine orthologue of human MSF, superficial zone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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             434
                                                                                374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 4; 34pp; English.
                                                                                                                                                                                                                          254
                                                                                                                                                                                                                                                                                                                                                                                                                                                983 PKDRATINSKATTPKPOKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRK-MTSTMPELNPT 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising the camptodactyly-arthropathy-coxavara pericarditis protein in combination with an anesthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Warman
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19-JUL-2000;
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dyyalskdqyynidvpsrtaraittrsgqtlsntwyncp 472
                    DYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1380
                                                                                                                                                            ALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRPE 1281
                                                                                                                                                                                                                                                                                \tt vrgpsqgfginpmfsdetnlcngrpvdglttlrngilvafrghyfwmltpftppppprri
                                                                     raigpsqvhtirihytpvrvpyqdkgflhnevkvstlwrglpnvvtsaislpnirkpdgy
                                                                                        RAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGY 1341
                                                                                                                                                                                                                               TEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVA 1221
                                                                                                                                       \verb"alslagyksrpesvyffkrggsvqgytykgeptqkctgrrpainysvygetagvrrrrfe"
                                                                                                                                                                                                           {\tt tevwgipspidtvftrcncegktfffkgsgywrftndikdagypkliskgfgglngkiva}
                                                                                                                                                                                                                                                                                                     PRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSDARRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoarthritis, or as lubricants of tissue and joints
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2000US-0145328
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79.9%; Pred. No. 2e-85;
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TCNCDY--NCQHYMECCPDFKRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDY 76

Matches

403;

Conservative

85;

Score 1188; DB 22; Pred. No. 4.9e-56; 85; Mismatches 536;

Indels Length

344;

Gaps

53;

Similarity

16.0%;

Sequence

5179 AA;

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The present invention describes colon tumour associated proteins (I) and (II) can be used in gene therapy and vaccine production. (I) and CI in any be used in the prevention, diagnosis and treatment of diseases casociated with inappropriate colon tumour associated protein (TCAP) concertifying mutations or deletions in a patient's genome that affect the patients own production of them. Additionally, (II) may be used to protect on the protein of them the protein or to supplement the produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences of similar nucleic acids in samples, and therefore which patients may be in need of restorative tharapy. (I) may can be used as DNA probes in diagnostic complementary sequences of similar nucleic acids in samples, and therefore which patients may be in need of restorative tharapy. (I) may can be used as one used as one activity. The anti-(I) antibodies against TCAPs anti-(I) antibodies and antagonists may also be used to down regulate cas diagnostic as antigens in the production of antibodies may also be used complementary capents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies may also be used complements for detecting the presence of TCAPs in samples and antagonists of the presence of TCAPs in samples cased to down regulate cased as diagnostic agents for detecting the presence of TCAPs in samples and antagonists may also be used to down regulate cased and Annial activity. The anti-(I) antibodies may also be used complements for detecting the presence of TCAPs in samples and antagonists may also be used as diagnostic agents for detecting the presence of TCAPs in samples cased complements for detecting the presence of TCAPs in samples cased complements for detecting the presence of TCAPs in samples can detecting the presence of TCAPs in the presence of TCAPs in the presen
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10-JAN-2000; 2000US-0480321
15-FEB-2000; 2000US-0504629
06-MAR-2000; 2000US-0519444
19-MAY-2000; 2000US-0575251
29-JUN-2000; 2000US-0509448
28-AUG-2000; 2000US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1999;
10-JAN-2000;
15-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colon tumor associated proteins and nucleic acids useful prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-441847/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C899P predicted amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
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E, Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 446-462;
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RARSULTIAN RARSOLTIID AAR800/11
IID AAR80 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             megakaryocyte; aplastic anaemia;
multipotential stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR80041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; megakaryocytopoientin;
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This sequence represents the human megakaryocytopoientin (MPO) protein
                                                                                                                                                          WPI; 1995-320576/41.
N-PSDB; AAT04546.
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                                                                                                                                                                                                                                                                                                                     04-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                               06-MAR-1995;
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                                            Example;
                                                                                                                                                                                                                                                                      (SHAN-) SHANGHAI BEITI BIOTECHNOLOGY CO
                                                                                      thrombocytopenia
                                                                                                           New haematopoietic cell growth factor
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                                                                                             and hematocytopenia
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ia; thrombocytopenia; hematocyto
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                       Bovine; CACP protein; camptodactyly-arthropathy superficial zone protein; SZP; MSF orthologue; costeoarthritis; joint lubrication; osteopathic;
                                                            Bos
                                                                                                                                                  Bovine MSF orthologue, superficial zone protein (SZP).
                                                                                                                                                                                                                                             AAB60569 standard; Protein;
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                              WO200107068-A1.
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                                                                                                                                                                                                                                                                                                                       tpkephpplprslhpptkepapttpkepaptapkkpaplpple 443
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83.5%;
                                                                                                         camptodactyly-arthropathy-coxa vara-pericarditis;
ein; SZP; MSF orthologue; synovial lubricant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2081; DB 16;
Pred. No. 9.3e-106;
3; Mismatches 21;
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                                                       Novel tribonectin polypeptide useful as lubricant for osteoarthritis, comprises O-linked lubricating moiety
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              Disclosure; Fig 1; 47pp; English
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of diagnosing osteoarthritis or a predisposition to osteoarthritis by comeasuring the amount of MSF or its fragment in a biological sample of a CC mammal, wherein an increased amount of MSF compared to a control CC indicates the presence of or predisposition to developing CC osteoarthritis. The tribonectin and DNA encoding it are useful in the CC treatment of osteoarthritis, where they may be used for lubricating CC mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is CC useful for inhibiting adhesion between two surfaces such as the injured ctissues of a mammal, where the injury is caused by a surgical insertion CC or trauma, or an artificial device e.g., an orthopaedic implant. In CC particular, one of the surfaces is pericardial tissue. DNA encoding a CC tribonectin may be used in gene therapy. The present sequence represents of a substantial portion of a human MSF-derived tribonectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1.76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method
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Page 1198-1201; 1275pp;
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CC The invention relates to a human tribonectin which is a product of CC alternative splicing of the human MSF (megakaryocyte stimulating factor) CC gene. The tribonectin has at least one O-linked oligosaccharide CC lubricating molety and has a polypeptide sequence comprising 1-76 CC repeats of a motif having at least 50% identity to the sequence KEPAPTT CC (AAB29774). The invention also relates to a nucleic acid encoding a CC human MSF-derived tribonectin; a biocompatible composition comprising a CC human MSF-derived tribonectin; a biocompatible composition and a method CC measuring the amount of MSF or its fragment in a biological sample of a CC measuring the amount of MSF or its fragment in a biological sample of a CC indicates the presence of or predisposition to developing CC indicates the presence of or predisposition to developing costeoarthritis. The tribonectin and DNA encoding it are useful in the treatment of osteoarthritis, where they may be used for lubricating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MSF; megakaryocyte stimulating factor; tribonectin; alternative splicing; joint boundary lubricant; O-linked oli osteoarthritis; tribosupplementation; tissue adhesion inhibiticition; coefficient reduction; gene therapy; antiarthritic;
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N-PSDB; AAC81498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents
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                                                              COXA vara-pericarditis (CACP) protein, or portions of the CACP protein.

CC The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous conjection. The human CACP protein is identified in the invention as composition the human CACP protein is identified in the invention as composition of the protein (MSF). The gene encoding composition of this gene are responsible for the heritable disorder camptodactyly-cc arthropathy-coxa vara-pericarditis, in which patients have synovial the protein (MSF) of the perilasia without evidence of inflammation. CACP protein (MSF) composition may be composed to reduce the symptoms of osteoarthritis. The composition may be composent human megaharyovyte stimulating factor (MSF, CACP protein). The sequence is not given in its entirety in figure 4 of the composition and therefore cheating factor (MSF, CACP protein).

CC segments human megaharyovyte stimulating factor (MSF, CACP protein). The composition and the composition of the composition of the composition and the composition of the composition and the composition of the composition of the composition and the composition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSF; megakaryocyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic; antiarthritic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathy. coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1999;
19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1;
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                                                           DCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKK 120
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Human megakaryocyt
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Peptide #90/	AAM14533	22	2665		446.5
C. albicans R	AAY05477	20	750		446.5
PRP encoused by cr	AAR14162	12	378		446.5
Human Okea Okea	AAB42491	21	3266		447.5
Streptococc	AAY81609	21	1237	6.0	448
ď	AAR14160	12	378		450.5
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atrophi	AAY17406	20	1012	6.1	Ď
de #1289 enc	AAM02607	22	511		467.5
#1349	AAM27312	22	511		σ
#L3L/	AAM14883	22	511		467.5
ard aar	AAP82974	9	652		476.5
Human protein sequ	AAB95541	22	1127		485
C900P predicted am	AAM24513	22	957		488
	AAY59288	21	957		488
de #286	AAM04187	22	617		488
1000	AAM16458	22	617		488
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uman SKCAP.	AAB50362	\sim	3118		489.5
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Protein encoded by	AAR10872	12	182	10.1	750

ALIGNMENTS

Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing. 02-FEB-1993 (first entry) /label= Exon_IV 157..200 /label= Exon_V 200..1141 /label= Exon_II 67..107 /label= Exon_I 26..67 Location/Qualifiers /label= Exon_VIII 1213..1266 /label= Exon_III 107..157 /label= Exon_IX /label= Exon_VII 1166..1212 411..1166 'label= Exon_VI



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Matches 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA coding for Plasmodium falciparum antigens - expressing poly:peptide(s) having antigenicity of RESA or FIRA antigens falciparum
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11-SEP-1984;
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N-PSDB; AAN60473.
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                                                           EKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPA----PTTP
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85AU-0047326.
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asegdnislsrlseeteek 842
                      AKPKDRATNSKATTPKPQK 985
                                               e---tvteqeptttqetvtaqepittqepvtaqepvttqeliatqepsttqe--hadekk
                                                                    KITATTTQVTSTTTQDTTPFK--ITTLKTTTLAPKVTT-----TKKTITTTEIMNKPEET
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                         This novel 55 kDa protein is encoded by an open reading frame of a Mycobacterium tuberulosis DNA fragment (see AAT93610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAM31851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for
                                                                                                                                                                                                                  New DNA and related proteins or RNA derived from M. tube used for diagnosis of mycobacterial infections, monitori vaccination and development of anti-mycobacterial agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ppapn--rppappap--pappel------pappdp----ptppvansppap
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                                                                                                           antigen;
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Pred. No. 1.7e-25;
                                                                                                                                                  Interspersed Repeat Antigen
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27-MAR-1986.

WO8601802-A

11-SEP-1985;

85WO-0006960

Plasmodium

falciparum

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RESULT :
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The present sequence is obtained from a clustral x alignment with protein 608. Protein 608 was identified using the method of the inventic after subjecting rat osteoblasts to mechanical stress. Expression of the 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue
                                                                                                                                                                                    WPI;
                                                                                                                Claim 32;
                                                                                                                                   Identification of stress induced genes for determining preventing, treating or controlling osteoporosis -
                                                                                                                                                                                                                                          (QUAR-)
                                                                                                                                                                                                                                                                     15-MAY-1998;
                                                                                                                                                                                                                                                                                               14-MAY-1999;
                                                                                                                                                                                                                                                                                                                         25-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mechanical stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence g1/1017427/emb/CAA62189 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKATTPKPQKP----TKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTM-----PELNP 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAIN
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                                                                                                                                                                                                                                          QUARK BIOTECH INC.
                                                                                                             Fig 6A-R; 308pp; English.
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                                                                                                                                                                                                             Skaliter R,
                                                                                                                                                                                                                                                                                                                                                                                                        ; gene therapy; protein 608; osteoporosis; bone density;
g1/1017427/emb/CAA62189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or bone density or other factors causing or contributing to osteoporosis or its symptoms or other conditions involved in mechanical stress or its lack. The methods can also be used for advancing research or studies in bone development. or cells comprising bone cells), isolating the specific cellular fractions and extracting mRNA from them, and differentially analysing mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identify bone development. to identify the

Sequence 4412 AA;

Query Match Best Local Sim Matches 258;

Similarity 23.8 58; Conservative

122;

Mismatches 464;

242;

Gaps

49

8.8%; Score 640; DB 21; 23.8%; Pred. No. 4.6e-26;

Length 4412; Indels

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                                       DKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT
                                                                            akvpevpkkpv----leekpavp---vperaespppevyee--peeiap---eeeiapee
                                                                                                                   --APTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTS
                                                                                                                                                       elppvkvpevpkevvpekkvplvvpkk--peappakvpevpkevvpekkvavpkkpevpp
                                                                                                                                                                                              EKPAPTTPEELAPTTPEEPTP-TTPEEPAPTTPKAAAPNTPKEPAP----TTPKEP----
                                                                                                                                                                                                                                   ppkpespppevfeepeevaleeppaevveepepaappqvtvppknpvpekkapavvakkp
                                                                                                                                                                                                                                                            PTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLT----PTTPEKLAPTT----P
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-eepevpppavpeepkkiipekkvp-vikkpeapppkepepekv---i 4009
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RESULT 1
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ID AAW3
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DT 27-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, monitoring vaccination, and for the development of vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccination and development of anti-mycobacterial agents
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, stagling, monitoring and prognosing diseases of the human breast particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
 Sequence
                                                                                                                                                                                                                         Claim 27; SEQ ID No 12385; 322pp; English.
                                                                                                                                                                                                                                                           Novel single exon nucleic acid in a human breast .
                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                              (MOLE-)
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                        ftp.wipo.int/pub/published_pct_sequences
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1325 AA;
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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Similarity

11.0%;

Score 802; DB 22; Pred. No. 2.5e-35;

Length 1325

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22-0CT-1999;
25-0CT-1999;
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25-0CT-1999;
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28-OCT-1999;
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26-OCT-1999;
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28-OCT-1999;
 C. thermocellum OlpB protein
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                                                        AAW43106;
                                                                                  AAW43106 standard;
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99US-0161993
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99US-0160768.
99US-0160770.
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Pred. No. 3.3e-45;
4; Mismatches 293;
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Multimer; enzyme; complex; protein-protein interaction; dockerin domain; cohesin domain; catalytic subunit; scaffold subunit; SdbA; synergistic; cellulosome integrating protein; scaffoldin dockerin binding protein.

Clostridium

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Cellulase proteins with cohesin or dockerin type II domains - of for potentiating the activity of multiprotein enzyme complexes
                                                                                                                                                                                                                                                                                                                                                                            Domain
Claim 7; Page 31-39; 60pp; French.
                                                                N-PSDB; AAT86623
                                                                                                           Beguin P,
                                                                                                                                                                  10-MAY-1996;
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useful

cc respectively. An example of such a complex is the cellulose degrading cc protein complex from Clostridium thermocellum, known as the cellulosome. Cc This complex comprises around 15 proteins including endoglucanases, cc ellubohydratases, hemicellulases, e.g. xylanases or lichinases, which cc interact with a central "scaffold" protein designated the cellulosome cc integrating protein (CipA; see AAW43108). The catalytic subunits compared to the cyrating protein (CipA; see AAW43108). The catalytic subunits compared to a protein invention relates to the isolation of proteins binding to a novel compared domain is designated a type II dockerin domain found on the catalytic subunits of the cype II dockerin found on the catalytic subunits of the cype II dockerin type compared to the type II dockerin domain found in the Creminal portion of Cip. The new compared to the catalytic subunits of the cellulosome). The type II dockerin domain for a protein which binds the novel type II dockerin domain and is the product of the OlpB gene. The protein contains 4 type II cohesin domains in the N-terminal portion of CipA. The nowel type II dockerin domain and is the product of the olpB gene. The protein contains 4 type II cohesin domains in the N-terminal portion of CipA. The novel type II dockerin domain and is the product of the olpB gene. The protein contains 4 type II cohesin domains in the N-terminal portion of CipA. The novel type II dockerin and cohesin domains in the N-terminal portion contains the protein which binds the protein contains the protein contains the protein contains and cohesin domains in the N-terminal portion contains the collaboration contains and cohesin domains in the N-terminal portion contains the collaboration contains compared contains contai Multimeric protein, especially enzymatic, complexes are held together by protein protein interactions between domains designated dockerins and cohesins, which are found on the catalytic and scaffold subunits respectively. An example of such a complex is the cellulose degrading in complexes, especially actions in a synergistic Sequence es, especially enzyme complexes, to potentiate their catalytic a synergistic manner. 1664 AA; The novel type II dockerin and cohesin domains

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                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                           thaliana protein
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                             2000EP-0301439
                                                                                    99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
99US-0128714.
              99US-0130449.
99US-0130510.
99US-0130891.
99US-0131449.
                                                                                                                                                 99US-0123548.
99US-0125788.
                                                             99US-0129845.
99US-0130077.
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   -0132048
                                                                                                                                                                                                                                                                                                                       genetic
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promoter;
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                                                                                                                                                                                                                                                                                                                                               cc administration of a composition comprising the camprodactyly-arthropathy-
cc coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.

CC The composition may further comprise a local namesthetic. The composition
cC of the invention may be administered via intra-articular or intravenous
cc injection. The human CACP protein is identified in the invention as
cc being megakaryocyte stimulating factor (MSF). The gene encoding
cc CACP protein (MSF) is located on chromosome 1q25-31, and mutations in
cc this gene are responsible for the heritable disorder camptodactyly-
cc arthropathy-coxa vara-pericarditis, in which patients have symovial
cc hyperplasia without evidence of inflammation. CACP protein (MSF)
cc acts as a synovium lubricant, and can be used to lubricate tissue and
cc joints in the treatment of osteoarthritis. The composition may be
cc applied to reduce the symptoms of osteoarthritis (e.g., joint pain,
cc loss of range of movement or joint damage). The present sequence
cc represents the bovine orthologue of human MSF, superficial zone
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              Matches
                      1148
                                                                                                                                                         1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, user treating osteoarthritis, or as lubricants of tissue and joints
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 4; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Warman
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19-JUL-2000;
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                                                      194
                                                                                                                                                                                                    969 PKDRATINSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRK-MTSTMPELNPT 1027
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                                                                                                                                                                                         76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a method of treating osteoarthritis via the
TEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVA
                                            s-lpeamlqtttrptptpnseildvnsenedgdaaegekphmifrppvltpivipgteil
                                                                                                                                SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL 1087
                                                                                                                                                                                  pkgratnsqvttpkpqkptkapkkptstkkprt-prvrkpkttptppktttsampeptpt
                                                                                                                                                                                                                                                                                                                                             472
                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0145328
2000US-0145328
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                                                                                                                                                                                                                                                       23.4%; Score 1707.5; DB 2; 79.9%; Pred. No. 1.7e-84; tive 24; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     superficial zone protein
                                                                                                                                                                                                                                                                                     DB 22; Length
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                                                                                                                                                                                                                                                                                        472;
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                                                                                 1147
                                                 253
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the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP). Cc expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by cc rectifying mutations or deletions in a patient's genome that affect the Cc patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cc cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in detect and the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs
                     RESULT
AAM24516
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10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                   The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity (I) and (II) can be used in gene therapy and vaccine production. (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                 King
                                                                                                                                                                                                                                                                                                                                                   Colon tumor
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                                                                                                                                                                                                                                                                                                   Claim 2; Page 446-462; 472pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C899P predicted amino acid
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                                                                                                                                                                                                                                                                                                                                    prevention,
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28-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunotherapy; diagnosis; colon cancer; colon tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                   GE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGY 1327
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E, Wang T
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                                                                                                                                                                                                                                                                                                                               associated proteins and nucleic acids useful for diagnosis and treatment of colonic cancer \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0480321.
2000US-05194629.
2000US-0519444.
2000US-0575251.
2000US-0609448.
2000US-0649811.
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                                                                                                                                                                                                                                                                                                                                                                                                              Secrist H,
Jiang Y;
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multipotential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human megakaryocytopoientin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1996
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  (SHAN-) SHANGHAI BEITI BIOTECHNOLOGY CO
                                             04-MAR-1994;
                                                                                       06-MAR-1995;
                                                                                                                                       08-SEP-1995
                                                                                                                                                                                 WO9523861-A1
                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVST
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                                                                                                                                                                                                                                                                                                                                                                 sapiens
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ryocyte; aplastic anaemia; thrombocytopenia; ho
otential stem cell.
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                                                                                            95WO-CN00015
                                                                                                                                                                                                                                                      444..446
                                                                                                                                                                                                                                                                                                 Location/Qualifiers 393..396
                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                           "unspecified amino acids"
                                                                                                                                                                                                                              "unspecified amino acids
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Matches 381
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                                                                                                                                                                                                                                                                                                                              KIKSSKNSAANRELQKKLKVKDNKKNRTKKKETPKPEVVDEAGSGLDNGDFKVTTPDTST
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                                                                                                                                                                                                      KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS
                                                                                                                                                                                                                                                                                                                                                                              ppsgasqtiksttkrspkppnkkktkkvieseeite---
epaptapkkpaplpple
                             EPAPTAPKKPAPTTPKE
                                                           aptttkshpplprscxxxxctqp-
                                                                                          APTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPK
                                                                                                                        \verb|ttpkeptpttiksapttpkepaptttksapttpkepaptttkepapttpkepaptttkep|
                                                                                                                                          TTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTIPKEPAPTTTKEPAPTTTKEPAPTTTKEP
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Pred. No. 8.2e-97;
3; Mismatches 21;
                                                             tpkephpplprslhpptkepapttpk
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                                                                                                   Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic;
23-APR-1999;
                                                                            Homo
                                                                                                                                                                                                               AAB29778 standard;
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                                                                            sapiens
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                                                                                                                                                                                                                                                                                                             RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEETAKPKDRATNSKATTPK
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                                                                                                                                                                                                                                                              ffkrggsiqqyiykqepvqkcpgrrpalnypvyge 1295
                                                                                                                                                                                                                                                                                                  rcncegktfffkdsgywrftndikdagypkpifkgfggltggivaalstakyknwpesvy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt tapttlkepapttpkkpapkelaptttkgptsttsdkpapttpketapttpkepapttpk}
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Query Match Best Local Sim Matches 794;

Similarity 74.6 94; Conservative

47.8%;

28;

Score 3484; D Pred. No. 9.6e 28; Mismatches

DB 22;

Length Indels

162;

Gaps

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The invention relates to a human tribonectin which is a product of CC alternative splicing of the human MSF (megakaryocyte stimulating factor) CC gene. The tribonectin has at least one O-linked ollyosaccharide CC lubricating molety and has a polypeptide sequence comprising 1-76 CC repeats of a motif having at least 50% identity to the sequence KEPAPTT CC (AAB29774). The invention also relates to a nucleic acid encoding a human tribonectin for inhibiting tissue adhesion formation; and a method CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a CC mammal, wherein an increased amount of MSF compared to a control CC indicates the presence of or predisposition to developing osteoarthritis. The tribonectin and DNA encoding it are useful in the treatment of osteoarthritis, where they may be used for lubricating CC mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured cor trauma, or an artificial device e.g., an orthopaedic implant. In CC particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents a substantial portion of a human MSF-derived tribonectin.
Sequence
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15-SEP-2000;
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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating f gene. The tribonectin has at least one O-linked oligosaccharide lubricating molety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KF (AAB29774). The invention also relates to a nucleic acid encoding
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N-PSDB;
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thuman MSF-derived tribonectin; a biocompatible composition comprising a CC human tribonectin for inhibiting tissue adhesion formation; and a method CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by CC measuring the amount of MSF or its fragment in a biological sample of a CC indicates the presence of or predisposition to developing cC indicates the presence of or predisposition to developing CC osteoarthritis. The tribonectin and DNA encoding it are useful in the CC treatment of osteoarthritis, where they may be used for lubricating CC mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is CC useful for inhibiting adhesion between two surfaces such as the injured CC tissues of a mammal, where the injury is caused by a surgical insertion CC or trauma, or an artificial device e.g., an orthopaedic implant. In CC particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents

Sequence 1404 AA;

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                                                     The invention relates to a method of treating osteoarthritis via the cadministration of a composition comprising the camptodactyly-arthropathy-cc coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous conjection. The human CACP protein is identified in the invention as the being megakaryocyte stimulating factor (MSF). The gene encoding cc CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-cc arthropathy-coxa vara-pericarditis, in which patients have synovial cc hyperplasia without evidence of inflammation. CACP protein (MSF) cats as a synovium lubricant, and can be used to lubricate tissue and conjunts in the treatment of osteoarthritis. The composition may be composed to the symptoms of osteoarthritis (e.g., joint pain, cc loss of range of movement or joint damage). The present sequence cc represents human megakaryocyte stimulating factor (MSF, CACP protein). CC sequence was therefore obtained from GenBank (U70316).
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tstttqdttpfkittlktttlapkvtttkktitttelmnkpeetakpkdratnskattpk
                                                                                                   KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT
                                                                                                                                              TAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK
                                                                                                                                                                                        APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG
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                     TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK
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                                                                 {\tt TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV
                                                                                      kpapttpetpppttsevstptttkepttihkspdestpelsaeptpkalenspkepgvpt
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                                                                                                                                                                                                                                                           Query Match 99.6%; Score 7265; DB 13; Length 1404; Best Local Similarity 97.3%; Pred. No. 0; Matches 1366; Conservative 0; Mismatches 0; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                               Sequence
Claim 1, 2 and 3; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human mega-karyocyte stimulating factors - for treating immune deficiencies, cancer, exposure to radiation or drugs, bacterial and viral infections, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark SC, Gesner TG,
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N-PSDB; AAQ27223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-1991;
10-SEP-1991;
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                                                                                     61 krvctaelsckgrcfesfergrecdcdaqckkydkccpdyesfcaevhnptsppsskkap 120
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91US-0757022.
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1373..14
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1331..1373
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В

260	KCNCEGKTEFEKDSOYWRFTMDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY 1	1201	Db VY
20	etnicngkpvdglttlrngtlvafrghyfwmlspfsppsparritevwgipspidtvft	14	В
16	CNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT 1	10	Qy
1140		œ	Db
, ,	TPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMDEVTPDMDVLDBVDNOGTTINDNIG 1	0	Ωy
1042		1021	Db 4
1020	tsttqdttpfkittlktttlapkvtttkktittteimnkpeetak	961	g B
982	TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK	923	Qy
σ .	tktpaatkpemtttakdktterdlrttpetttaapkmtketatttektteskitatttqv	901	Db
ผ	TKTPAATKPEMTTTAKOKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV	863	Qγ
862 900	kpapttpetpppttsevstptttkepttihkspdestpelsaeptpkalensokepgypt	841	망 .
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- 0	tapttlkepapttpkkpapkelaptttkqptsttsdkpaptrpketapttpkcpaptrpk	781	망
	TAPTILKEPAPTIPKKPAPKELAPTTTKGPTCTTTCAKOKTTTCKETTTTTTCTTTTTTTTTTTTTTTTTTTTTTTT	743	ρ
780		721	DЬ
	APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTBKC	683	γQ
		661	рь
, α	PEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP	623	Qy
σ 1	aptapkepapttpketapttpkkltpttpeklapttpekpapttpeelapttpeeptptt	601	Db
N	APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT	563	Qy
	ttksapttpkepsptttkepapttpkepapttpkkpapttpkepapttpkepaptttkkp	541	В
Ď	TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKK	503	Qy
	epaptapkkpapttpkepapttpk	481	Db
õ	PAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAP		Qy
480	aptttksapttpkepapttpkkpapttpkepapttpkeptpttpkepapttkepapttpk		Db
-	PTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTP	œ.	Qy
N i	ttpkeptpttiksapttpkepaptttksapttpkepaptttkepapttpkepaptttkep	36	ф
œ	PKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKE	\sim	Qy
σ .		0	Db
N	EKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEF	6	Qy
0 0	tdhnkvstspkittakpinprpslppnsdtsketsltvnkettvetketttnkqtstdq	24	Дb
j.	3 TOHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKOTST	0	Qy
-		18	Db
202	3 KIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTS	14	Qy

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
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Copyright (c) 1993 - 2000 Compugen Ltd
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Human EST encoded
Human MSF-derived
Human megakaryocyt
Bovine MSF ortholo
                                                                                                                                                                                                                                                                                Description
                          C899P predicted am
Arabidopsis thalia
C. thermocellum Ol
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Human megakaryocyt
       Peptide #2327 enco
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AAM26950	4	AAB42491	AAB40945	AAY 05477	AAR14162	AAY81609	AAR14160	AAY17406	AAB35408	AAM02607	AAM27312	AAM14883	AAP82974	AAB95541	51	AAY59288	AAM04187	AAM16458	AAR26042	AAB50362	AAB50363	AAB41231	AAR10872	AAB11727	AAW48299	AP82975	AAB11726	AAY54466	AAY54467	AAP60570		AAY53666	6.3
	#007	* 0.5	X T G	Uman ORFY ORF709	This are by	Streptococcus paca	TRE STOR ILLECTOR	Human acropati i i	Hullian 0/CGZ/ yene	Peptide #1209 enco	Peptide #1080 Grac	Peptide #1310 open	Broadnesive precur	Hulldi process sega	Cytop predicted am	MUCTI POT	de #200	1000	#3007	Hall BACAF.	SECAP.	CRCAD ORF	בו פון	OF CLAP	rod	Bloadnesive precur		Amino acid sequenc	DICTO	Ce or	rer rum	sequence gi/ioi/42	eriu

ALIGNMENTS

Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing.

RESULT

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Kegion	Bogion		Region		Region		Region		Region		Region		Region		Region		Region	Key		Synthetic.		stability; pro	Megakaryocyte		MSF precursor.		02-FEB-1993 (AAR26049;	AAR26049 standard;	
/label= Exon_IX	1213 . 1266	/label= Exon_VIII	11661212	/label= Exon_V11	14111166	/Label= Exon_vi	2001141	/ Laber = Exon_v	157200	/label= Exon_iv	_	/label= Exon_iii		/label= Exon_11		/label= Exon_1		Location/Quartifiers				stability; proteolytic cleavage;	colony stimulating				(first entry)			Procein; 1404	1101
		H																ers				adhesion; dicernative apric	ractor; secretion signar, m							3.	

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                                              injection. The human CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-arthropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) acts as a synovium lubricant, and can be used to lubricate tissue and joints in the treatment of osteoarthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence represents human megakaryocyte stimulating factor (MSF, CACP protein). Note: This sequence is not given in its entirety in figure 4 of the specification, although a GenBank accession number was given. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1381 psrtaraittrsgqtlskvwyncp 1404
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                                                                                                                                                                                                                                                                                    coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; MSF; megakaryocyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of treating osteoarthritis via the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1999; 99US-0145328.
19-JUL-2000; 2000US-0145328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200107068-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human megakaryocyte stimulating factor (MSF, CACP).
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                                      sequence was therefore obtained from GenBank
                                                                                                                                                                                                                                                                                                                                           administration of a composition comprising the camptodactyly-arthropathy-
                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page ~; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                treating osteoarthritis, or as lubricants of tissue and joints
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warman ML;
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Sequence

1404 AA;

Ouery Match Best Local Sinilarity 99.34, Score 7265; DB 22; Length 1404; Best Local Sinilarity 99.34, Score 7265; DB 22; Length 1404; Best Local Sinilarity 99.34, Score 7265; DB 22; Length 1404; Best Local Sinilarity 99.34, Score 7265; DB 22; Length 1404; Best Local Sinilarity 99.34, Score 7265; DB 22; Length 1404; Best Local Sinilarity 99.34, Score 7265; DB 22; Length 1404; 29 1
watchs 1366; Conservative 0; Hammatches 0; Indels 38; Gaps 1266; Conservative 0; Hammatches 0; Indels 38; Gaps 1404; Hammatches 0; Indels 30; Gaps 1404; Hammatches 0; Indels
Match 99.5%; Score 7265; Db 22; Length 1404; 10coal Similarity 97.3%; Pred: Mo. 0; Indels 38; Gaps 1 AMKTIPIYLLLLSVEVIQOYSSOLISCAGROGESTRDATCNCDYNCQHYMCCCPDF 60 1
tch 1365; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1366; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1366; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1367; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1368; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1368; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1368; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1368; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1468; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1479; Conservative 97.3%; Pred: No. 0; Indels 38; Gapp 1489; Conservative 97.3%;

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Region

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The sequence given is a full length translation from the megakaryocyte contribution of the megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, contributed in the megakaryocyte stimulating factor (MSF). This contributed is modified by the addition of an N-terminal sequence encoding content of the form human megakaryocyte colony stimulating factor (msg. CSF). Exon I contains the initiating methionine, and encodes a colassical mammalian protein sedvention signal sequence. The sequence conding the original meg-cSF includes exons II-IV and is thought to terminate in the region between amino acid residues 134 - 147. The contributed in the region between amino acid residues 134 - 147. The contributed in the region between amino acid residues 134 - 147. The contributed in the region between amino acid residues 134 - 147. The contributed in the region between amino acid residues 134 - 147. The contributed in the region between amino acid residues 134 - 147. The contributed in the region between amy be cleaved in different ways to contribute of this gene may be cleaved in different ways to contribute of the stability, folding and processing of the contributed in the stability, folding and processing of the contributed in the processing or folding to play a role in the observed contributed in the processing or folding of the appropriate structure of the resulting factor, ie. one or more of these exons may contain contributed processing or folding of the appropriate structure of the cellular matrix or extracellular matrix processing. Both naturally coccuring MSF s may be characterised by various combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different axis.
      Query Match
Best Local S
Matches 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human mega-karyocyte stimulating factors - for immune deficiencies, cancer, exposure to radiation
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10-SEP-1991;
                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterial and viral infections, etc.
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/label= Exon_XI

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97.38;
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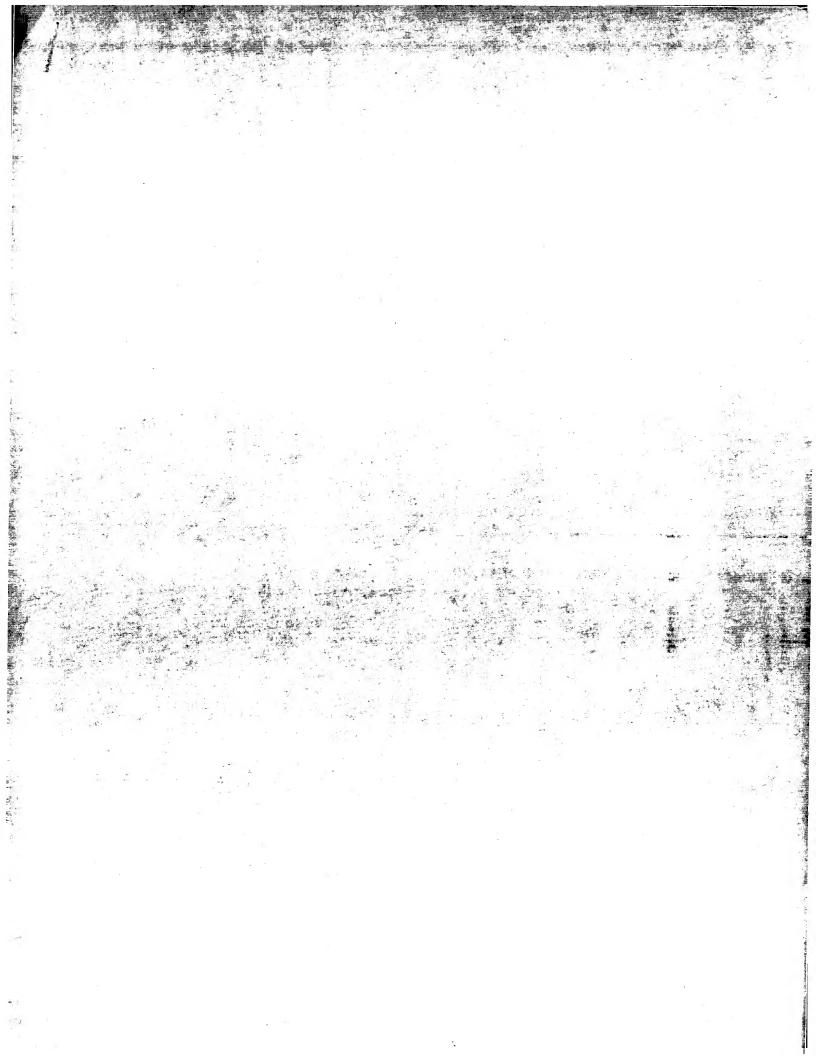
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Amino acid sequenc Cryptosporidium pa Bioadhesive precur Cryptosporidium pa Portion of Cryptos Protein encoded by Human ORFX ORF995

Sequence of the Fa

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GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score: Sequence: 1 MAWKTLPIYLLLLLSVEVIQ......ARAITTRSGQTLSKVWYNCP 1366

OM protein - protein search, using sw model

April 26, 2002, 16:24:52; Search time 138.84 Seconds (without alignments) 728.782 Million cell updates/sec

Run on:

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters:

522463

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Human 07CG27 gene Human atrophin-1 r PRP 378. Triticum

Human SRCAP. Homo Human SRCAP. Homo P. yoelil SSP2 ant Peptide #2892 enco Peptide #2869 enco

ALIGNMENTS

Streptococcus pneu pRP encoded by clo C. albicans Rbtl p Human ORFX ORF709 Human ORFX ORF2255 Peptide #967 encod Peptide #987 encod

RESULT AAR26049 AAR26049 standard; Protein; 1404 AA.

02-FEB-1993 (first entry)

AAR26049;

MSF precursor.

Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing.

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Peptide #987 Peptide #941 Human ORFX OR	39 Japanese sea m 08 Human 07CG27 go 33 Peptide #967 en	477 C. ablicans RbtT p 559 Caenorhabditis ele 566 Caenorhabditis ele	Bload Pept Pept Pept Pept Pept Pept Pept Pept	8 Human MC11 po 3 C900P predicte 9 Cryptosporidite 1 Human protein	2 Mycoba 5 Sequen 6 Sequen 7 Sequen 7 Amini 6 Amino 6 Crypto 6 Crypto 6 Human 1 Human 1 Human 2 Portio 9 Peptid 7 Peptid	page 1. , database: A-Genesey-1101

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                       The sequence given is a full length translation from the megakaryocyte stimulating factor (MSF) procursor. The sequence covered by exons II., CC III.and IV encodes megakaryocyte stimulating factor (MSF). This CC sequence is modified by the addition of an N-terminal sequence encoding a secretory leader, an initiating methionine proceeding exon II and a C terminating codon following exon IV. The CDNA sequence given contains, CC sequences derived from human megakaryocyte colony stimulating factor (Meg-CSF): Exon I contains the initiating methionine, and encodes a C classical mammalian protein secretion signal sequence. The sequence cc encoding the original meg-CSF includes exons II-IV and is thought to terminate in the region between amino acid residues 134 - 147. The CC yield a family of mRNA's each encoding a different MSF protein. Exons CC yield a family of mRNA's each encoding a different MSF protein. Exons CC yield a family of mRNA's each encoding a different MSF protein. Exons CC yield a family of the stability, folding and processing of the CC molecule. These exons are also thought to play a role in the observed CC synergy of MSF with other cytokines. Exons V - XII are believed to be resulting factor, ie. one or more of these exons may contain CC sequences which direct proteolytic cleavage, adhesion, organisation of the cellular matrix or extracellular matrix processing. Both naturally CC various combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different XX members of the MSF family.
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                                                                                                                                                                                                                        Query Match 98.5%; Score 6470.5; Best Local Similarity 87.5%; Pred. No. 0; Matches 1229; Conservative 0; Mismatches
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905 1080	PQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN		p dq
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785	TTAAPKMTKETATTTEKTTESKITATTTQV	726	p
960		901	Qy
725	KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT	666	Db
900		841	dq
665	PTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK	606	Db 04
840		781	
605	TTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG	546	DB Qy
780		721	
545	AAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP	486	DP GA
720		661	
485	APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT	426	Db
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365	TTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT	306	D Q
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                             CC administration of a composition comprising the camptodactyly arthropathy-
CC coxh vara-pericarditis (CACP) protein, or portions of the CACP protein.
CC The composition may further comprise a local anaesthetic. The composition
CC of the invention may be administered via intra-articular or intravenous
CC injection. The human CACP protein is identified in the invention as
CC being megakaryocyte stimulating factor (MSF). The gene encoding
CC CACP protein (MSF) is located on chromosome 1925-31, and mutations in
CC this gene are responsible for the heritable disorder camptodactyly-
CC arthropathy-coxa vara-pericarditis, in which patients have synovial
CC hyperplasia without evidence of inflammation. CACP protein (MSF)
CC cts as synovium lubricant, and can be used to lubricate tissue and
CC joints in the treatment of osteoarthritis. The composition may be
CC applied to reduce the symptoms of osteoarthritis (e.g., joint pain,
CC loss of range of movement or joint damage). The present sequence
CC represents human megakaryocyte stimulating fatory (MSF, CACP protein).
CC represents human megakaryocyte stimulating fatory (MSF, CACP protein).
CC sequence is not given in its entirety in figure 4 of the
CC specification, although a GenBank accession number was given. This
CC sequence was therefore obtained from GenBank (UV)316).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   treating osteoarthritis,
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                                                                                                                                                                                                                                                                                                                                             invention relates to a method of treating osteoarthritis via the inistration of a composition comprising the camptodactyly-arthropa
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or as lubricants of tissue and joints
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                AAR26049
AAB60568
AAB29778
AAB29778
AAB29778
AAR80041
AAB60516
AAR38942
 AAM03645
                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522463
                                     Human megakaryocyt
Bovine MSF ortholo
C899P predicted am
Arabidopsis thalia
                                                                                                         MSF precursor. Sy
Human megakaryocyt
Human megakaryocyt
Human EST encoded
Human MSF-derived
                                                                                                                                                                                                                    Description
   Peptide #2327 enco
                      thermocellum Ol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aa7.rag
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AAR26049

ID AAR2

XX AAR2

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XX M2-F

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XX Mega
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ (D; I, a) AAR 26049, Dadabase: A. Genescy-1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR26049 standard; Protein; 1404 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR26049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSF precursor
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Human atropnin-1 r			101	6.1		45
C. albicans koti P	0 AAY05477		750	6.1		44
PRP encoded by CLO			378	6.1	446.5	43
Human Oxfr A Oxfr 4000			326	6.1	449.5	42
reprise #941 encod			2665	6.1	449.5	41
#98/			266	6.1	449.5	40
			2665	6.1	449.5	39
			37	6.2	450.5	38
			281	6.2	451	37
		1 22	511	6.4	467.5	36
#1349			51	6.4	467.5	ω G
Peptide #131/ enco	2 AAM14883		51	٠	7	34
ve pre	AAP82974		65	6.5	476.5	ω ω
Human protein sequ			112	•	485	32
C900P predicted am			95	6.7	488	31
Human MUC11 polype			95	6.7	488	30
Peptide #2869 enco			61	6.7	488	29
2687			. 61		488	28
1 SSP			82	6.7	488.5	27
Human SRCAP. Homo			311		489.5	26
•			297		489.5	25
Human ORFX ORF995			297	6.8	496.5	24
Portion of Cryptos			172		496.5	23
Cryptosporidium pa			172	6.8	496.5	22
Bioadhesive precur	Þ		744	6.9	506.5	21
Cryptosporidium pa			183	7.0	510.5	20
Amino acid sequenc			781	7.1	520.5	19
Amini acid sequenc			80.	7.4	542	18
Sequence of the Fa	AAP60570	7	844		552.5	17
Mycobacterium tube			572	8.4	612	16
MSF-K130. Synthet			11:			15
91			441	8.8	643	14
Mycobacterium tube	AAW3185	3 18	763		715	L I
Protein encoded by	AAR10872		187	10.3	756	12
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ALIGNMENTS

(first entry)

FT Region FT Region FT Region FT Region FT Region	KW Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; KW stability; proteolytic cleavage; adhesion; alternative splicing. XX XX XX XX XX XX XX XX XX
67.107 /label= Exon_III 107.157 /label= Exon_IV 157.200 /label= Exon_V 200.1141 /label= Exon_VI 1411.1166 /label= Exon_VII 1166.1212 /label= Exon_VIII	yte pro
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                                                                                                                                                                                                                                                                             The sequence given is a full length translation from the megakaryocyte Stimulating factor (MSF) precursor. The sequence covered by exons II, CC ILI and IV encodes megakaryocyte stimulating factor (MSF). This CC sequence is modified by the addition of an N-terminal sequence encoding CC a secretory leader, an initiating methionine proceeding exon II and a C terminating codon following exon IV. The cDNA sequence given contains Sequences derived from human megakaryocyte colony stimulating factor (Meg-CSF). Exon I contains the initiating methionine, and encodes a CC classical mammalian protein secretion signal sequence. The sequence chooling the original meg-CSF includes exons II-IV and is thought to complete the region between amino acid residues 114 - 147. The CC primary transcript of this gene may be cleaved in different ways to CC wand VI are thought to be related to the activity of the factor and CC molecule. These exons are also thought to play a role in the observed CC implicated in the stability, folding and processing of the resulting factor, ie. one or more of these exons may contain CC the resulting factor, ie. one or more of these exons may contain Sequences which direct proteolytic cleavage, adhesion, organisation of the cellular matrix or extracellular matrix processing. Both naturally CC various combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chaim 1, 2 and 3; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1992.
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                                                                                                                                                                                                                                                                           equence
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D-SEP-1991;
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   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by human mega-karyocyte stimulating factors - for treating mmune deficiencies, cancer, exposure to radiation or drugs, acterial and viral infections, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              egion
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                                                                                                                                                                                            Local Similarity hes 1361; Conservat
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                                                                                                                            1/MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992-284660/34.
                                                                             KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNDTSPPSSKKAP 120
PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITE------------
                                                         {\tt krvctaelsckgrcfesfergrecdcdaqckkydkccpdyesfcaevhnptsppsskkap}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gesner TG,
                                                                                                                                                                                                                                                                           1404 AA;
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91US-0757022
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/label= Exon_X
1331..1373
/label= Exon_XI
1373..1404
/label= Exon_XII
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                                                                                                                                                                                                             Score 7291.5;
Pred. No. 0;
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                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                          DB 13; Length 1404;
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                                                                                                                                                                                          Indels 43; Gaps
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Qу ДЪ	Db Qy	dq Vy	Фр	Дy	ДУ	Оy	QУ	Оу	Оу	Оу	Оу	Qy	Qy Db	Qy	ОУ	Qу Дъ	Qy dd
1158 1201		38 81	978 1021	961	858 901	798 841	738 781	678 721	618	0 5	498 541	38 81	378 421	318 361	258 301	198 241	157 181
RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY 121 	DETNICNGKPYDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTYFT 115 	QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVEMPEVTPDMDYLPRVPNQGIIINPMLS 109 	PQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN 103 	TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK 977 	TKTPAATKPEMTTTAKDKTTERDLRITPETTTAAPKMTKETATTTEKTTESKITATTTQV 917 	KPAPTIPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 857	TAPTILKEPAPTTPKKPAPKELAPTITKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK 797 	APTTTKEPTSTTSDKPAPTTPKGTAPTTPKE 	EPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKETAPI 	PTTPKKLTPTTPEKLAPTTPEKPAPT] 	SPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAP; 	APTTPKEPAPTTTKEPSPTTPKEPAPTTT 	KEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEI 	SAPTTPKE sapttpke	KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS 317 	TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTINKQTSTDG 257 	YKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST 197
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BRACK SAME BRACKS AND SOLUTION STATES AND SOLUTION SOLUTIONS SOLUT
                                        The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.

The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous in lection. The human CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSE). The gene encoding CACP protein (MSE) is located on chromosome 1925-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-carthropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSE) acts as a synovium lubricant, and can be used to lubricate tissue and complied to reduce the symptoms of osteoarthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, class of range of movement or joint damage. The present sequence constitution and complete in the treatment of osteoarthritis (e.g., joint, pain, class of range of movement or joint damage. The present sequence constitution in the composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint, pain, class of range of movement or joint damage. The present sequence constitution in the present sequence constitution in the sequence of the sequence was therefore obtained from GenBank (UT)316).
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      eguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eating osteoarthritis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w composition comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cample 1; Page -; 34pp; Engli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    man; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; regukaryocyte stimulating factor; synovial lubricant; romosome 1925-31; osteoarthritis; joint lubrication; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rman ML;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the camptodactyly-arthropathy-coxa a combination with an anesthetic, useful for as lubricants of tissue and joints
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	18 PEPAPTIPKAAARNTPKEPAPTIPKEPAPTTPK. 61 Peepapttpkaaapntpkepapttpkepapttpkepapttpkepapttpkepapttpk) B &
	58 APTARKEPAPTTPKETAPTTPKKLTÖTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPT 6	9 dg 04
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1;	ery Match 99.6%; Score 7291.5; DB 22; Length 1404; st Local Similarity 96.9%; Pred. No. 0; tches 1361; Conservative 0; Mismatches 0; Indels 43; Gaps	Qu Ma

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Listing first 45 summaries
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DB seq length: 2000000000
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Match
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 MSF precursor. Sy Human megakaryocyt Human megakaryocyt Human EST encoded Human MSF-derived Human MSF-ortholo C8999 predicted am Arabidopsis thalia C. thermocellum Ol Peptide #2327 enco
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272	AAT UD4/			6.5	456.5	37
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Peptide #13	AAP829/4	ی د	652	6.7	476.5	ω ω
artection and the contraction of	AAB95541	22		6.9	485	32
uman prote	AAW48299	19		6.9	488	31
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_ ^	AAM04187	22		6.9	488	28
Peptide #20	AAM16458	22		6.9	488	27
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ortion	AAB11727	21		6.9	489	25
Human SKCAP	AAB50362	22		6.9	489.5	24
	AAB50363	22		6.9	489.5	2
Human CRFX	AAB41231	21		7.0	496.5	22
MSF-K130.	AAR26050	13		7.0	498	21
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	AAB11726		183	7.2	508	19
Amino acia	AAY54466		78	7.4	520.5	18
Protein enco	AAR10872	12	182	7.5	529	17
Amini acid	446	21	807	7.7	542	16
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Palapage Topy

Cryptosporidium pa Bioadhesive precur MSF-K130. Synthet Human ORFX ORF995 Portion of Cryptos p. yoelli SSP2 ant peptide #2892 enco peptide #2869 enco Sequence of the Fa Amini acid sequenc Protein encoded by Mycobacterium tube Sequence gi/101742 Mycobacterium tube Human SRCAP. Amino acid sequenc Homo

ALIGNMENTS

PRP encoded by clo Caenorhabditis ele Caenorhabditis ele Japanese sea musse Human 07CG27 gene EYFP-DEVD-MAP4-EBF

Bifunctional casps

Cryptosporidium pa Human protein sequ Bioadhesive precur Peptide #1317 enco Peptide #1349 enco Peptide #1289 enco Peptide #1289 enco C. albicans Rbti p PRP 378. Triticum

Human MUC11 polype C900P predicted am

AAR26049 standard; Protein; 1404 AA. Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing. MSF precursor 02-FEB-1993 (first entry) /label= Exon_I 26..67 Location/Qualifiers /label= Exon_II

1166..1212 /label Exon_VIII 1213..1266

/label- Exon_VI 1411..1166

/label= Exon_VII

200..1141

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                                                                                                                                                                                                                                                                stimulating factor (MSF) precursor. The sequence covered by exons II, cili and IV encodes megakaryocyte stimulating factor (MSF). This contains the initiating methionine proceeding exon II and a terminating codon following exon IV. The cDNA sequence given contains terminating codon following exon IV. The cDNA sequence given contains sequences derived from human megakaryocyte colony stimulating factor (meg-CSF). Exon I contains the initiating methionine, and encodes a classical mammalian protein secretion signal sequence. The sequence encoding the original meg-CSF includes exons II-IV and is thought to terminate in the region between amino acid residues 134 - 147. The pylimary transcript of this gene may be cleaved in different ways to yield a family of mRNA's each encoding a different MSF protein. Exons V and VI are thought to be related to the activity of the factor and are also implicated in the stability, folding and processing of the implicated in the processing or folding of the appropriate structure of the resulting factor, ie. one or more of these exons may contain concurring and non-naturally occurring MSF's may be characterised by curious combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different and the sequence, with the exons spliced together in differing orders to form different and the sequence, with the exons spliced together in differing orders to form different and the sequence.
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N-PSDB; AAQ27223.
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human mega-karyocyte stimulating factors - for inmune deficiencies, cancer, exposure to radiation bacterial and viral infections, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₩ф9213075-А.
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10-SEP-1991;
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hes 1311; Conservative
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93.4%; Pre
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Qy 1108 RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTG
Qy 1048 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPF
988 QTPNSKLVEVNPKSEDAGGAEGETPH
28 PQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTP
868 TST 961 tst
08 TKT
748 KPA 841 kpa
688 TAP 781 tap
628 APT 721 apt
58 PEE 51 pee
508 APT 601 apt
Qy 448 TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPT
388 EPA 481 epa
328 APT 421 apt
268 TTF 361 ttp
208 KEK 301 kek
48 TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETS
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                                                                                                                                                                                                                                                                      Example 1; Page -; 34pp;
                                                                                                                                                                                                                                                                                          New composition comprising the camptodactyly-arthropathy-coxavana-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint.
                                                                                                                                                                                                                                                                                                                                                                             E
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19 JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarthrit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; CACP protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                   protein (MSF) is located on chromosome 1925-31, and mutations in gene are responsible for the heritable disorder camptodactyly-propathy-coxa vara-pericarditis, in which patients have synovial as a synovium lubricant, and can be used to lubricate tissue and place to reduce the symptoms of osteoarthritis. The composition may be soft range of movement or joint damage). The present sequence is not given in its entirety in figure 4 of the efficient of the symptoms of osteoarthritis (MSF, CACP protein).
                        pence
 ence
                                                                                                                                                                       invention relates to a method of treating osteoarthritis via the unistration of a composition composition the camptodactyly-arthropathy-avara-pericarditis (CACP) protein, or portions of the CACP protein, composition may further comprise a local anaesthetic. The composition he invention may be administered via intra-articular or intravenous pection. The human CACP protein is identified in the invention as
                                                                                                                                                                                                                                                                                                                                                                            man ML;
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                   was therefore obtained
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Mycobacterium tube Sequence 91/101742 Mycobacterium tube

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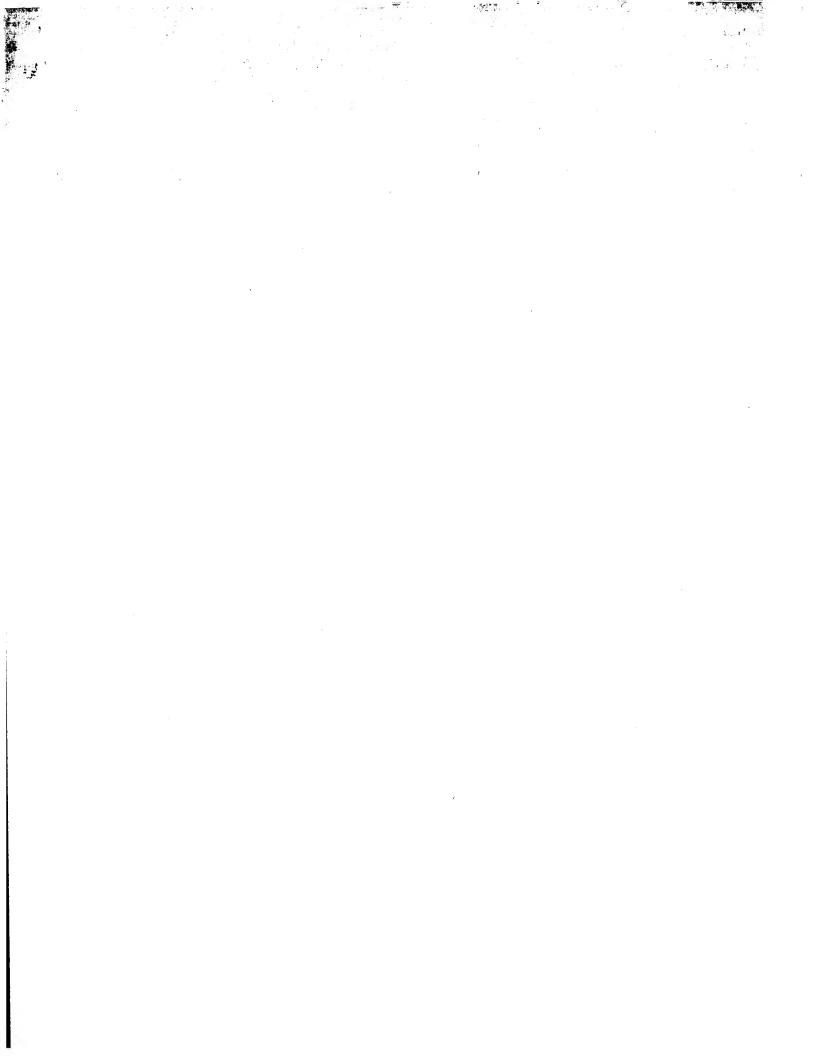
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ALIGNMENTS

RESULT	II.T. 1
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Ħ	AAR26049 standard; Protein; 1404 AA.
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ΑC	AAR26049;
XX	
ρŢ	02-FEB-1993 (first entry)
XX	
DE	MSF precursor.
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KW	Megakaryocyte colony stimulating factor; secretion signal: megicsf:
ΧW	adhesion: alternative spli
×	
SO	Synthetic.
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FH	Key Location/Qualifiers
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FΤ	/label= Exon_I
FT	Region 2667
FT	/label= Exon_II
FT	Region 67107
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	Match 99.6%; Score 7245.5; DB 13; Length 1404; Local Similarity 97.1%; Pred. No. 0; es 1363; Conservative 0; Mismatches 0; Indels 41; Gap	17-JAN-1992: 92WO-US00433. 18-JAN-1992: 92WO-US00433. 18-JAN-1992: 91US-0643502. 10-SEP-1991: 91US-0643502. 10-SEP-1991: 91US-0757022. (CERMY) GENETICS INST INC. CLAIK SC. Gesner TG, Hewick RM, Jacobs K, Turner K; WPI: 1992-284660/34. NPSDB; AAQ27223. NPW human mega-karyocyte stimulating factors - for treating fumume deficiencies, cancer, exposure to radiation or drugs, bacterial and viral infections, etc. CLAIM 1, 2 and 3; Fig 1; 87pp; English. The sequence given is a full length translation from the megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, sequence is modified by the addition of an N-terminal sequence and intitating methionine proceeding exon I and a terminating codon following exon IV. The cDNA sequence given contains the intitating methionine, and encodes a sequencing the original meg-CSF includes exons II I'V and is thought to this gene may be cleaved in different ways to yeld a family of mRNA's each encoding a different MSF protein. Exons V and VI are thought to be related to the activity of the factor and a sequence with other yelds in the stability, folding and processing of the squences of MSF with other cytokines. Exons V - XII are believed to be the resulting factor, as one on more of these propopriate structure of sequences which direct proteolyric cleavege, adhesion, organisation of counting and non-raturally cocuring way sequences. Sequences of the MSF family.	Region 12661331 /label= Exon_X Region 13311373 /label= Exon_XI Region 13731404 /label= Exon_XI

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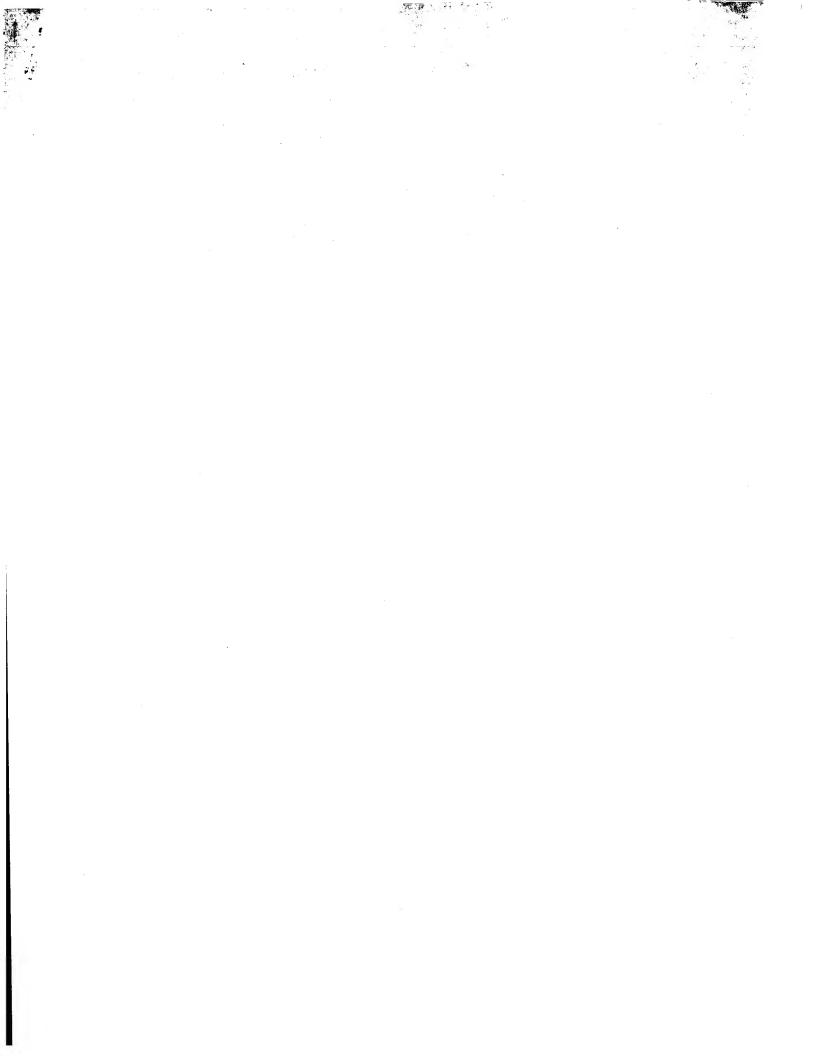
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The invention relates to a method of treating osteoarthritis via the campinatorial content of a composition combrising the campinatory of arthropathy-cox avara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered to a intra-articular or intravenous the injection. The human CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSF). The gene encoding this gene are responsible for the heritable disorder campiodactyly-car thropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) and mutations in the sas a synovium lubricant, and can be used to lubricate tissue and joints in the treatment of osteoarthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, caprisents human, megakaryocyte stimulating factor (MSF, CACP protein). Whise sequence is not given in its entirety in figure 4 of the specification, although a denama can and through a sequence was therefore other and from Company (1770746).
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Arabidopsis thalia
C. thermocellum 01
Peptide #2327. enco
                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                              MSF precursor.
Human megakaryı
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	#987	Peptide #967 encod	Bifunctional caspa	EYEP-DEVD-MAP4-EHE	Human 07CG27 gene	_	Caenorhabditis ele	Caenorhabditis ele	PRP encoded by clo	378. Triticu	cans Rb	Peptide #1289 enco		Peptide #1317 enco	Bioadhesive precur	Human protein secu	Sportdium	† T	21.5	#2869	Peatide #2892 enco	P. voelii ssp2 ant	Portion of Cryptos	SRCAP	٦ ;	Human ORFX ORF995	Bioadhesive precur	mulphroase	2	Amini acid sequenc	Sequence of the Fa	Mycobacterium tube	_	Mycobacterium tube	

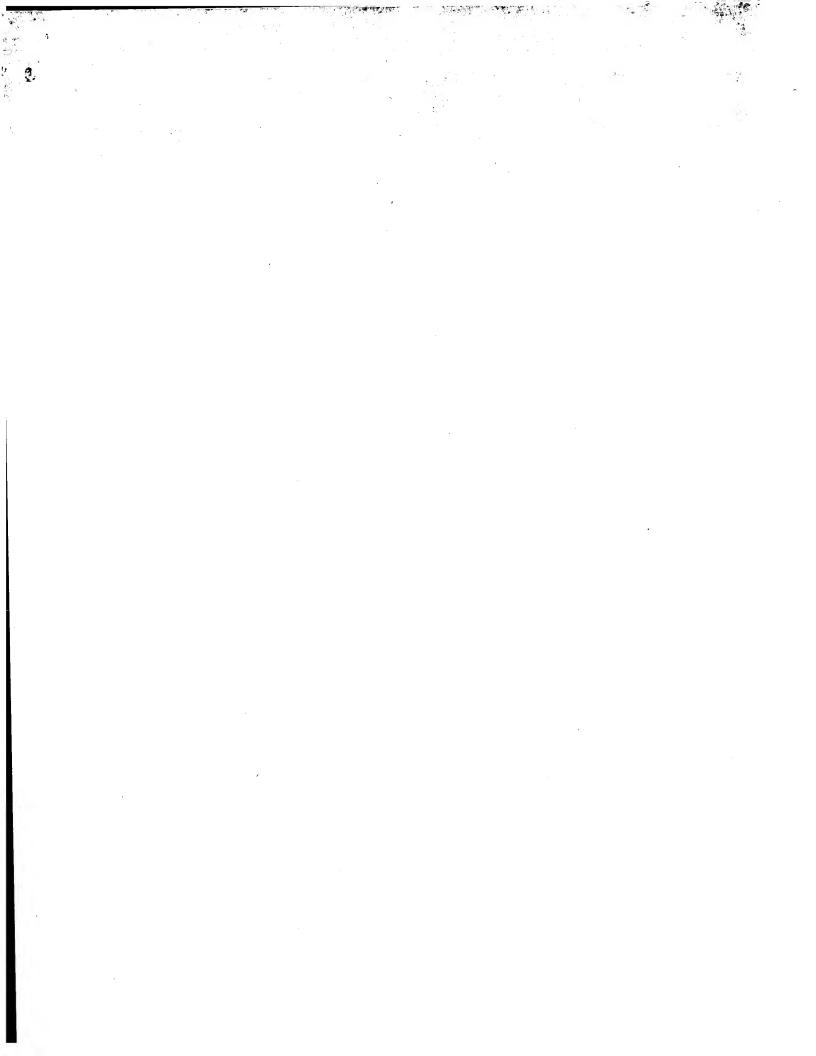
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	Region		Region		Region		Region		Region		Region		Region		Region		Region	Key		Synthetic.		stability; pr	Megakaryocyte	rock Procureous	MSF Dracingor	02-FEB-1993		AAK26049;		26049	AAR26049	RESULT 1
/label= Exon_IX	12131266	/label- Exon_VIII	11661212	. /label= Exon_VII	14111166	/label- Exon_VI	2001141	/label- Exon_v	157200	/label- Exon_IV	107157	/label= Exon_III	67107	/label= Exon_II		/label= Exon_I	126	Location/Qualifiers	-		atternative spilicing.		Megakaryocyte colony stimulating factor: secretion signal: megaces.	•	1	(first entry)				standard; Protein; 1404 AA.		

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                                                                                                                                                                                                                                        The sequence given is a full length translation from the megakaryocyte is stimulating factor (MSF) precursor. The sequence covered by exons II, considered by the addition of an N-terminal sequence in codified by the addition of an N-terminal sequence encoding terminating codon following exon IV. The cDNA sequence given contains the initiating methionine proceeding exon II and a sequences derived from human megakaryocyte colony stimulating factor (Meg-CSF). Exon I contains the initiating methionine, and encodes a concoding the original meg-CSF includes exons II-IV and is thought to primary transcript of this gene may be cleaved in different ways to the calculate in the region between amino acid residues 134 - 147. The color of this gene may be cleaved in different ways to are also implicated in the stability, folding and processing of the synergy of MSF with other cytckines. Exons V - XII are believed to be realiting factor, it come or more of these exons may contain the calcular matrix or extracellular matrix processing. Both naturally farious comminations of alternatively spliced exons from this sequence, the members of the MSF family.
                                                                                                                                                                        Matches 1270;
                                                                                                                                                                               t Local Similarity
h21 ppsgasqtiksttkrspkppnkkktkkvieseeiteehsvsenqesssssssssssstiw 180
                                            66
                                                   61 krvctaelsckgrcfesfergrecdcdaqckkydkccpdyesfcaevhnptsppsskkap 120
                                                               equence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1, 2 and 3; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human mega-karyocyte stimulating factors - for treating immune deficiencies, cancer, exposure to radiation or drugs, bacterial and viral infections, etc.
                                                                                                  Clark SC, Gesner TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-1991;
10-SEP-1991;
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0; Mismatches
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                       arthropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) aces as a synovium lubricant, and can be used to lubricate tissue and applied to reduce the symptoms of osteoarthritis. The composition may be loss of range of movement or joint damage. The present sequence workers human megakaryocyte stimulating fractor (MSF, CACP protein). Specification, although a GenBank accession number was given. This sequence was therefore obtained from GenBank (V70316).
                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathy-coke vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further compaise a local anaesthetic. The composition of the invention may be administeded via intra-articular or intravenous injection. The human CACP protein is identified in the invention as habing magnetarycours attenuation as the invention as
                                                                                                                                                                                                                                                                                                   injection. The human CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the her table disorder camptodactyly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page -; 34pp; Eng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising the camptodactyly-arthropathy-coxa vara pericarditis protein in combination with an anesthetic, useful for treating osteoarthritis, on as lubricants of tissue and joints
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ps and research use -

.aim 20; Page 1198-1201; 1275pp; English

prensics, gene mapping, lodiversity and for nutr cotein of the invention. the present invention provides the protein and coding sequences of novel coteins from a variety of organisms, including human, dog, cat, horse, w, pig, hawster, monkey, macaque, yeat, bacteria, fruit fly, sea chin and towato. These were derived from expressed sequence tags (ESTs) om the organism of interest. They can be used in diagnostics, remaics, gene mapping, identification of mutations, to assess odiversity and for nutritional purposes. The present sequence is a

equence 1299 A

Quer Best Matc Local Similarity hes 941; Conserva Match Conservat! 100.0%; 100.0%; tve 0 0, Score 5011; bB 22; Pred. No. 1.5e-273;); Mismatches 0; Indels Length 1299; 0 Gaps 0

61 õ PRPSLPPNSDTSKETSLTVNNETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK 120 vkdnkknrtkkkptpkppv\deagsgldngdfkvttpdtsttqhnkvstspkittakpin 259 VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPIN 60

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00 40 2 PTTPKEPAPTTKEPSPTTPKEPAPTTTKSAPTTKEPAPTTTKSAPTTPKEPSPTTTKE PKKPAPTTPKEPAPTTPKEPTPTTPKEPAPY pkkpapttpkepapttpkeptpttpkepaptt epapttpkepaptapkkpapttpkepa epaptttksapttpkepsptttke 559 360 499

TKEPAPTTPKEPAPTAPKKPAPTTPKEPA

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80 20 21 PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPÅPTTPKKPAPKELAPTTTK 540 TPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPYTPEEPAPTTPKAAAPNTPKE papttpkepapttpkepapttpketapttpkgtapttlkepap tpkkltpttpeklapttpekpapttpeelapttpeeptpt peepapttpkaaapntpke 679 480

EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAP :tpkkpapkelaptttk 799 600 739

kelaptttkgptsttsdkpapttpketapttpkepapttpkkpapttp KELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTÅPETPPPTTSEVST eptsttsdkpapttpkgtapttpkepapttpkepapttpkgtapt lkepapttpkkpap tpppttsevst 720 859 660

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 $\tt ptttkepttlhkspdestpelsaeptpkalenspkepgvpttktpaatkpdmtttakdkt$ PTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKREMTTTAKDKT

TERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPPKITTLKTT

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RESULT AAR26049 N

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TLAPKVTTYKKTITTEIMNKPEETAKPKDRAINSKATTPKPQKPTKAPKKPTSTKKPKT 840 terdikttpetttaapkmtketatttektteskitatttqvtstttqdttpfkittlktt 979

ttteimnkpeetakpkdratnskattpkpqkptkapkkptstkkpkt 1039

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980 tlapkvtttkk

841 MPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGG 900

ştmpelnptsriaeamlqtttrpnqtpnsklvevnpksedagg 1099

AAR26049 standard; Protein; 1404 AA.

AAR26049;

02-FEB-1993 entry

MSF precursor

Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing.

FIN SOX XX XX Synthetic.

Region Region Region Region Region Key Region Region Region Region Region Region /label- Exon_I 26..67 Location/Qualifiers 'label= Exon_VII 'label = Exon_II label = Exon_III label= Exon_VI label- Exon_V label = Exon_IV ..1141 el- Exon_x ...1373 .1331 200 Exon_VIII

WO9213075-A.

Region

/label= Exon_XI

Exon_XII

17-JAN-1992; 06-AUG-1992 92WO-US00433

18-JAN-1991; 10-SEP-1991; 91US-0643502 91US-0757022

GEMY) GENETICS INST INC

Clark SC, Gesner TG, Hewick ₽¥, Jacobs

WPI; 1992-284660/34. N-PSDB; AAQ27223.

New human mega-karyocyte stimulating factors for treating

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cc The sequence given is a full length translation from the megakaryocyte cc III and IV encodes megakaryocyte stimulating factor (MSF). This cc sequence is modified by the addition of an N-terminal sequence encoding cc tarminating codon following exon IV. The cDNA sequence given contains cc sequences derived from human megakaryocyte colony stimulating factor (MSF). Exon I contains the initiating methionine, and encodes a cc encoding the original meg-CSF includes exons II-IV and is thought to encoding the original meg-CSF includes exons II-IV and is thought to tarminate in the region between amino acid residues 134 - 147. The cc yield a family of mRNA's each encoding a different MSF protein. Exons cc yield a family of mRNA's each encoding a different MSF protein. Exons cr also implicated in the stability, folding and processing of the synergy of MSF with other cytokines. Exons V - XII are believed to be resulting factor, ie. one or more of these exons may contain the resulting factor, ie. one or more of these exons may contain of the cellular matrix or extracellular matrix processing. Both naturally cc wallous combinations of alternatively spliced exons from different cc with the exons spliced together in differing orders to form different cc mathematics of the members of the MSF family.
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ilarity 100.0%;
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Pred. No. 1.6e-273;
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      The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition
                                                                                 New composition comprising & vara-pericarditis protein in treating osteoarthritis, or a
                                                            Example 1; Page -; 34pp;
                                                                                                                                                                                                                                                                                                      Human;\CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; MSF; megakaryccyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
                                                                                                                                                                   (UYCA-) UNIV
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19-JUL-2000;
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he present invention provides the protein and coding sequences of novel coteins from a variety of organisms, including human, dog, cat, horse, w, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea tchin and tomato. These were derived from expressed sequence tags (ESTs) om the organism of interest. They can be used in diagnostics, yene mapping, identification of mutations, to assess ordiversity and for nutritional purposes. The present sequence is a Laim solat quence odiversity and for nutrotein of the invention. ·PSDB; ted polypeptide for treatment odies and research use -AAH98981 Page 1198-1201; 1299 ξ 1275pp; English Ģ, diseases, diagnostics, raising

Best Best Local Similarity Matches 968; Conserv _ Match prvative 100.0%; 0 Score 5155; DB 22; Pred. No. 3.9e-282; Mismatches 0 Indels Length 0 Gaps 0

EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKBPAPTTPKGTAPTTLKEPAPTTPKKPAP 739 600

KELAPTITKGPISTISOKPAPITPKETAPTTPKEÅPTIPKKPAPTIPETPPPTISEVST kelaptttkgptsttsdkpapttpketapttpkepapttpkkpapttpetpppttsevst 799

VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPIN 60

vkdnkknrtkkkp tpkppvvdeagsgldngdfkvttpdtsttqhnkvstspkittakpin

밁 Š

EPAPTITKSAPTTPKEPAPTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT dlaptskvlakptpkae thtkgpalttpkeptpttpkepasttpkeptptt1ksapttpk

| PKKPAPTTPKEPAPTTPKEPT\TTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPA

tpkkltpttpeklapttpekpapttpeelapttpeeptpttpeepapttpkaaapntpke

eptsttsdkpapttpkgtapttpkepapttpkepapttpkgtapttlkepapttpkkpap

PTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPDVPTTKTPAATKPEMTTTAKDKT

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TERDLATTPETTTAAPKMIKETATTTEKTTESKITATTTQVTSTTTQDTTPPFKITTLKTT

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919 859 660

SEQ ID NO: 1 AC NO: AAR26049, A-genesey_1101

밁 δ 밁 Ş 밁 Š 밁 Š 밁 1160 1100 1040 961 901 841 980 920 781 GTLVAFRG TLAPKVTTT AEGETPHMLLRPHVFMPEVYPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRN aegetphmllrphvfmpevtp mprvrkpkttptprkmt! MPRVRKPKTTPTPRÄMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGG tlapkvtttkkt% terdirttpetttaapkmtketatttektteskitatttqvtstttqdttpfkittlktt 979 1167 968 KKTITITEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKT 840 ttte1mnkpeetakpkdratnskattpkpqkptkapkkptstkkpkt 1039 tmpelnptsriaeamlqtttrpnqtpnsklvevnpksedagg ndylprvpnqgiiinpmlsdetnicngkpvdglttlrn 1159

1099 900

960

RESULT AAR26049 N

AAR26049 standard; Protein; 1404 æ

AAR26049;

02-FEB-1993 (first

MSF precursor

stability; Megakaryocyte /te colony stimulating
proteolytic cleavage; factor; secretion signal; meg-CSF; adhesion; alternative splicing.

Synthetic.

Region кеу Region Region Region Region Region Region /label= Exon_II 67..107 200..1141 /label= E /label-'label- Exon_V /label- Exon_III /label- Exon_I Location/Qualifiers 57..200 label Exon_IV el= Exon_VI Exon_VII

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W09213075-A

06-AUG-1992

92WO-US00433

18-JAN-1991; 10-SEP-1991; 91US-0643502 91US-0757022

(GEMY) GENETICS INST INC

Clark SC, Gesner TG, Hewick RM, Jacobs K, Turner

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The sequence given is a full length translation from the megakaryocyte contains from the megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, CC III and IV encodes megakaryocyte stimulating factor (MSF). This color is modified by the addition of an N-terminal sequence encoding cc sequence is modified by the addition of an N-terminal sequence encoding cc terminating codon following exon IV. The cDNA sequence given contains cc sequences derived from human megakaryocyte colony stimulating factor (MEG-CSF). Exon I contains the initiating methionine, and encodes a color original meg-CSF includes exons II-IV and is thought to cendoing the original meg-CSF includes exons II-IV and is thought to comminate in the region between amino acid residues 134 - 147. The cc violating transcript of this gene may be cleaved in different ways to comminate in the region between amino acid residues 134 - 147. The cc violating and implicated in the stability, folding and processing of the area also implicated in the stability, folding and processing of the cc sydergy of MSF with other cytokines. Exons V - XII are believed to be considered in the processing or folding of the appropriate structure of the resulting factor, it one or more of these exons may contain cc sequences which direct proteolytic cleavage, adhesion, organisation of the cellular matrix or extracellular matrix processing. Both naturally ccurring MSF's may be characterised by with the exons spliced together in differing orders to form different xxx
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New composition comprising the camptodactyly-arthropathy-coxavara-pericarditis protein in combination with an anesthetic, treating osteoarthritis, or as lubricants of tissue and joint
                                                                                                                                                                                                                                                                                23-JUL-1999;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
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proteins from a variety of organisms, including human, dog, cat, horse, cdw, pig) hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, gene mapping, identification of mutations, to assess idediversity and for nutritional purposes. The present sequence is a urotein of the invention. KELAPTITKGPTSTISDKPAPTIPKETAPTTPKEPAPTIPKKPÅPTTPETPPPTISEVST EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKdTAPTTLKEPAPTTPKKPAP papttpkepapttpkepapttpketapttpkgtapttlkkpapttpkkpapkelaptttk PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK 540 PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPT DLAPTSKVLAKPTPKAETTTROPALITPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPK 180 PRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK PTTPKEPAPTTTKEPSPTTPKEPAPTTTK\$APTTTKEPAPTTTKSAPTTPKEPSPTTTKE epaptttksapttpkepaptttkep\pttpkepaptttkepaptttksapttpkepaptt EPAPTTTKSAPTTPKEPAPTTTKÅPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT dlaptskvlakptpkaetttkgmalttpkeptpttpkepasttpkeptpttiksapttpk papttpkepapttpkkpapttpkepapttpkepaptttkkpaptapkepapttpketapt pkkpapttpkepapttpkeptpttpkepapttkepapttpkepaptapkkpapttpkepa $\tt prpslppnsdtsketsltv hattvetkettttnkqtstdgkekttsaketqsiektsak$ pttpkepaptttkepspttpkepaptttksapttkepaptttksapttpkepsptttke for treatment of diseases, diagnostics, rch use -Score 5416; DB 22; Pred. No. 2.4e-298; Mismatches English. Indels Length 0 499 600 300 240 660 799 679 480 619 420 559 360 379 319 120 259 0 밁 밁 Š 밁 Š 밁 δÃ 밁 Region 1160 Megakaryocyte colony stimulating factor; secretion signal; stability; proteolytic cleavage; adhesion; alternative spl: 1100 1040 Region Region Region Region Region Region Region Region Region Synthetic 02-FEB-1993 AAR26049 standard; MSF precursor 901 980 920 781 TLAPKYTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKT MPRVRKPKTTPXPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGG terqlrttpetttaapkmtketatttektteskitatttqvtstttqdttpfkittlktt 979 aegetphmllrphvfmpevt mprvrkpkttptpr tlapkvtttkktittteimnkpeetakpkdratnskattpkpqkptkapkkptstkkpkt 1039 (first 'label= Location/Qualifiers /label = Exon_II labellabel Exon_IV label- Exon_III Protein; mtstmpelnptsriaeamlqtttrpnqtpnsklvevnpksedagg el = Exon_x ..1373 el- Exon_VI l- Exon_VII .1212 200 l= Exon_IX .1331 Exon_VIII Exon_XI Exon_V Exon_I **d**mdylprvpnqgiiinpmlsdetnicngkpvdglttlrn 1404 3

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1992-284660/34

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The sequence given is a full length translation from the megakaryocyte Stimulating factor (MSF) precursor. The sequence covered by exons II, III and IV encodes megakaryocyte stimulating factor (MSF). This CC sequence is modified by the addition of an N-terminal sequence encoding CC a secretory leader, an initiating methionine proceeding exon II and a C terminating codon following exon IV. The cDNA sequence given contains CC (meg-CSF). Exon I contains the initiating methionine, and encodes a conditing the original meg-carretion signal sequence. The sequence CC encoding the original meg-cSF includes exons II-V and is thought to terminate in the region between amino acid residues 134 - 147. The CC yield a family of mRNA's each encoding a different ways to yield a family of mRNA's each encoding a different way by the color of the factor and molecule. These exons are also thought to play a role in the observed synergy of MSF with other cytokines. Exons V XII are believed to be the resulting factor, ie. one or more of these exons may contain of the cellular matrix or extracellular matrix processing. Both naturally variable and non-naturally occuring MSF; may be characterised by with the exons spliced together in different this sequence, with the exons spliced together in differing orders to form different the secons of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different to the MSF family.
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Best Local Similarity
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        New composition comprising the vara-pericarditis protein in of treating osteoarthritis, or as
                                                                                                                                                                                                                                                                                  23-JUL-1999;
19-JUL-2000;
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te camptodactyly-arthropathy-coxa combination with an anesthetic, a combination with an anesthetic, a label of tissue and joint.
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                                                                                                                                                                            ns from a variety
                                         lg, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea and tomato. These were derived from expressed sequence tags (ESTs) are organism of interest. They can be used in diagnostics, lcb, gene mapping, identification of mutations, to assess ersetty and for nutritional purposes. The present sequence is a of the invention.
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                                                                                                                                                                                                                                                                                                             for treatment of diseases, diagnostics, raising
                                                                                                                                             rovides the protein and coding sequences of of organisms, including human, dog, cat, however, macaque, yeast, bacteria, fruit fly, sea
                                                                                                                                                                                                                                              English
                                                                                                                                                                     horse,
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Ouery Match 100.0%; Best Local Similarity 100.0%; Matches 1064; Convervative 500 440 301 380 181 320 121 241 260 61 DLAPTSKYLAKPTPKAEÅTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPK pttpkepaptttkepspttpkepapttdksaptttkepaptttksapttpkepsptttke $\begin{array}{c} \texttt{PKRPAPTTPKEPAPTTPKEPTTPKEPAPTTKEPAPTTPKEPAPT$ EPAPTTTKSAPTTPKEPAPTTYKEPAPTTPKEPAPTTTKSPAPTTTKSAPTTPKEPAPTT PTTPKEPAPTTTKEPSPTTPKEPAPTÅIKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE pkkpapttpkepapttpkeptpttpkepapttkepapttpkepaptapkkpapttpkepa PRPSLPPNSDTSKEÅSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK 120 epaptttksapttpkepaptttkepapttpkepaptttkepaptttksapttpkepaptt prpslppnsdtskets tvnkettvetketttnkqtstdgkekttsaketqsiektsak 0, Score 5698; Pred. No. 0; Mismatches B 22; 0; Length 1299; 0; 559 499 300 360 240 180 379 319 60 259

721 860 661 900 601 740 541 481 421 560 361 TPKKLTPTTPEKLAPTTPEKPAPTTPEELAP\TPEEPTFTTPEEPAPTTPKAAAPNTPKE TERDLRTTPETTTAAPKHIKETATTTEKTIESKITATTTQVTSTTQQDTTPFKITTLKTT ptttkepttihkspdestpelsaeptpkalenspkepgvpttktpaatkpemtttakdkt kelaptttkgptsttsdkpapttpketapttpkepapttpl KELAPTITKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVST EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKETAPTTLKEDAPTTPKKPAP PTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTÅKTPAATKPENTTTAKDKT 720 eptsttsdkpapttpkgtapttpkepapttpkepapttpkgtapttlkepapttpkkpap papttpkepapttpkepapttpketapttpkgtapttlkepapttpkkpapkelaptttk PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAVTTLKEPAPTTPKKPAPKELAPTTTK 540 papttpkepapttpkkpapttpkepapttpl epaptttkkpaptapkepapttpketapt {kpapttpetpppttsevst 919 660 799 480 679 619 420 0

> RESULT AAR26049 밁 Ş 밁 밁 Š 밁 ő 밁 Ş 밁 1160 1220 1021 1100 1040 961 901 841 980 920 781 N TNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFK 1064 GTLVAFRGHYFWMLSPFSPPSPARRÌQEVWGIPSPIDTVFTRCNCEGKTEFFKDSQYWRF 1020 tndikdagypkpifkgfggltggivaalstakyknwpesvyffk 1263 gtlvafrghyfwmlspfsppsparrite\wgipspidtvftrcncegktfffkdsgywrf MPRVRKPKTTPTPRKKTSTMPELNPTSRIAEAMLOTTTRPNQTDNSKLVEVNPKSEDAGG TLAPKYTTTKKTITTTEIMKKPEETAKPKDRATNSKATTPKPOKPTKAPKKPTSTKRPKT mprvrkpkttptprkmts tlapkvtttkkt terdlrithetttaapkmtketatttektteskitatttqvtstttqdttpfkittlktt 979 tteimnkpeetakpkdratnskattpkpqkptkapkkptstkkpkt 1039 mpelnptsriaeamlqtttrpnqtpnsklvevnpksedagg 1099 1159 840

Synthetic Megakaryocyte stability; pro AAR26049 standard; Protein; 1404 AA MSF precursor yte colony stimulating factor; secretion signal; meg-CSF;
proteolytic cleavage; adhesion; alternative splicing. (first entry) Location/Qualifiers

Region Region Region Region Region Key Region Region Region Region Region /label= 1373..14 /label= 1331..13 /label- Exon_I 26..67 'label• 'label= Exon_III '07..157 .57..200 label Exon_IV labellabellabel Exon_II el- Exon_VI .1331 .1= Exon_XI .1266 :l= Exon_VII Exon_X Exon_IX Exon_VIII Exon_V

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18-JAN-1991; 10-SEP-1991; 17-JAN-1992; 91US-0643502 91US-0757022 92WO-US00433

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CC III and IV encodes megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, contains the incidence of the addition of an N-terminal sequence encoding terminating codon following exon IV. The cDNA sequence given contains code encoding terminating codon following exon IV. The cDNA sequence given contains code encoding the original megakaryocyte colony stimulating factor codes a encoding the original megakaryocyte colony stimulating factor codes a encoding the original megakaryocyte colony stimulating factor codes a encoding the original megacyte includes exons II-IV and is thought to colony transcript of this gene may be cleaved in different ways to primary transcript of this gene may be cleaved in different ways to complete the factor and code molecule. These exons are also thought to the activity of the factor and code are also implicated in the stability, folding and processing of the code synergy of MSF with other cytokines. Exons V - XII are believed to be the resulting factor, ie. one or more of these exons may contain code code in the coding of the appropriate structure of the cellular matrix or extracellular matrix processing. Both naturally cocuring and non-naturally occuring MSF's may be characterised by well and processing of the members of the MSF family.

CC with the exons spliced together in differing orders to form different to the members of the MSF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 1064;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                        1 VKDNKKNRTKKKPTPKPPVVDBAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPIN
sequence given is a full lengt
mulating factor (MSF) precursor
                                                                   pttpkepaptttkepspttpkepaptttksaptttkepaptttksapttpkepsptttke
                                                                                    PTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE
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                                                                                                                                    pkkpapttpkepapttpkeptpttpkepapttkepapttpkepaptapkkpapttpkepa
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                                                                                                                                                                                                                                                                     {\tt dlaptskvlakptp} {\tt kaetttk} {\tt gpalttpkeptpttpkepasttpkeptpttiksapttpk}
                                                                                                                                                                                                                                                                                         DLAPTSKYLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPK
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megakaryccyte stimulating factor; synovial lubricant;
mosove 1q25-31; osteoarthritis; joint lubrication; osteopathic;
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SEA 10 NO: 1, 25-/404 Pa

ACNO: AAR 260A9, A-Geneser-1101

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
April 26, 2002, 16:15:40 ; Search time 107.17 Seconds
(without alignments)
953.822 Million cell updates/sec

Title: US-09-556-246-1_COPY_25_1404 Perfect score: 7410

Perfect score: 7410
Sequence: 1 QDLSSCAGRCGEGYSRDATC.....ARAITTRSGQTLSKVWYNCP 1380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

522463

522463 seqs, 74073290 residues

Searched:

cimum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: A_Geneseq_1101:*
1: /SIDS8/gcgdata/geneseq/yeneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/yeneseqp/AA1981.DAT:*
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28: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

O	Query Match	Length	DB	Ī	Description
7410	100.0	1404	13	AAR26049	MSF precursor. Sy
7410	100.0	1404	22	AAB60568	Human megakaryocyt
7410	100.0	1404	22	AAB29773	Human megakaryocyt
6834	92.2	1299	22	AAM24322	Human EST encoded
3484	47.0	902	22	AAB29778	Human MSF-derived
2081	28.1	452	16	AAR80041	Human megakaryocyt
1707.5	23.0	472	22	AAB60569	Bovine MSF ortholo
1188	16.0	5179	22	AAM24516	C899P predicted am
981	13.2	763	21	AAG38942	Arabidopsis thalia
950	12.8	1664	19	AAW43106	C. thermocellum Ol
805	10.9	1325	22	AAM03645	Peptide #2327 enco
	•	Query Match 100.0 100.0 100.0 97.2 47.1 28.1 16.0 16.0 113.2 113.2	Query Match 100.0 100.0 100.0 92.2 47.0 16.0 113.2 113.2 110.9	Query Match Le 100.0 100.0 100.0 92.2 47.0 28.1 23.0 16.0 13.2 12.8 10.9	Ouery Match Length DB I 100.0 1404 13 100.0 1404 22 100.0 1404 22 47.0 902 22 47.0 902 22 47.1 452 16 23.0 472 22 16.0 5179 22 13.2 763 21 12.8 1664 19 10.9 1325 22

Peptide #987 encod	AAM26950	22	2665	6.0	446.5	45
Peptide #967 encod	AAM14533	22	2665	6.0	446.5	44
C. albicans Rbtl p	AAY05477	20	750	6.0	446.5	43
	AAR14162	12	378	6.0	446.5	42
Human ORFX ORF2255	AAB42491	21	3266	6.0	447.5	41
Streptococcus pneu	AAY81609	21	1237	6.0	448	40
PRP 378. Triticum	AAR14160	12	378	6.1	٠	39
Human 07CG27 gene	AAB35408	22	2819	6.1	454.5	38
Human atrophin-1 r	AAY17406	20	1012	6.1	•	37
Peptide #1289 enco	AAM02607	22	511	6.3	•	36
	AAM27312	22	511	6.3	467.5	35
	AAM14883	22	511	6.3	467.5	34
Bioadhesive precur	AAP82974	9	652	6.4	476.5	ω u
Human protein segu	AAB95541	22	1127	6.5	485	32
C900P predicted am	AAM24513	22	957	6.6	488	31
Human MUC11 polype	AAY59288	22	957	6.6	488	30
Peptide #2869 enco	AAM04187	22	617	6.6	488	29
Peptide #2892 enco	AAM16458	22	617	o. 6	488	28
P. yoelii SSP2 ant	AAR26042	13	826	6. 6	488.5	27
Human SRCAP. Homo	AAB50362	22	3118	6.6	489.5	26
Human SRCAP. Homo	AAB50363	22	2972	6. 6	489.5	25
Human ORFX ORF995	AAB41231	21	2971	6.7	496.5	24
Cryptosporidium pa	AAW48299	19	1721	6.7	498	23
Portion of Cryptos	AAB11727	21	1721	6.7	498.5	22
Bioadhesive precur	AAP82975	9	744	6.8	506.5	21
	AAB11726	21	1837	6.9	513	20
-	AAY54466	21	788	7.0	520.5	19
Amini acid sequenc	AAY54467	21	807	7.3	úл	18
Sequence of the Fa	AAP60570	7	844	7.5	555.5	17
Mycobacterium tube	AAW31855	18	572	8.3	612	16
MSF-K130. Synthet	AAR26050	13	111	8.3	613	15
Sequence g1/101742	AAY53666	21	4412	8.7	645.5	14
Mycobacterium tube	AAW31852	18	763	9.6	715	<u>1</u> 3
Protein encoded by	AAR10872	12	182	10.1	752	12

ALIGNMENTS

F	FT	FΤ	FT	FΤ	Ħ	ĘŢ	Ä	Ţ	ΓŢ	Ţ	ΕŢ	Ţ	FΤ	Ţ	Ħ	ĘŢ	ΕŢ	FH	×	SO	×	Χ¥	X	×	D	X	멹	×	AC.	×	H	RESULT
	Region		Region		Region	-	Region		Region		Region		Region		Region		Region	Key		Synthetic.		stability; pro	Megakaryocyte		MSF precursor.		02-FEB-1993 (AAR26049;		ID AAR26049 stand	ET 1
/label= Exon_IX	12131266	/label= Exon_VIII	11661212	/label- Exon_VII	14111166	/label= Exon_VI	2001141	/label- Exon_V	157200	/label= Exon_IV	107157	/label- Exon_III	67107	/label= Exon_II	2667	/label- Exon_I	126	Location/Qualifiers					Megakaryocyte colony stimulating factor; secretion signal; meg-CSF;				(first entry)				AAR26049 standard; Protein; 1404 AA.	

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CC III and IV encodes megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, CC sequence is modified by the addition of an N-terminal sequence encoding a secretory leader, an initiating methionine proceeding exon II and a CC terminating codon following exon IV. The CDNA sequence given contains CC (meg-CSF). Exon I contains the initiating methionine, and encodes a CC classical mammalian protein secretion signal sequence given contains CC eriminate in the region between amino acid residues 134 - 147. The CC primary transcript of this gene may be cleaved in different ways to CC yield family of mRNA's each encoding a different MSF protein. Exons CC v and VI are thought to be related to the activity of the factor and care also implicated in the stability, folding and processing of the cellular matrix or extracellular matrix processing. Both naturally cocuring and non-naturally occuring MSF's may be characterised by CC various combinations of alternatively spliced exons from this sequence, with the exons spliced together in different this sequence, with the exons spliced together in differing orders to form different CC members of the MSF family.
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10-SEP-1991;
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administration of a composition comprising the camptodactyly arthropathy-
CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein.
CC The composition may further comprise a local anaesthetic. The composition
CC of the invention may be administered via intra-articular or intravenous
CC injection. The human CACP protein is identified in the invention as
CC cacp protein (MSF) is located on chromosome 125-31, and mutations in
CC this gene are responsible for the heritable disorder camptodactyly-
CC arthropathy-coxa vara-pericarditis in which patients have synovial
CC hyperplasia without evidence of inflammation. CACP protein (MSF)
CC acts as a synovium lubricant, and can be used to lubricate tissue and
CC ions of range of movement or joint damage). The present sequence
CC note: This sequence is not given in its entirety in figure 4 of the
CC specification, although a Genbank accession number was given. This
CC sequence was therefore obtained from Genbank (U70316).
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